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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
1801 AGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCA 1842
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CURRENT FILING DATE: 2001-07-12
PRIOR PAPLICATION NUMBER: WCT/US00/04414
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
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PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21309
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
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PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR PILING DATE: 1999-12-07
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Sequence 118, Application US/09905125A
Patent No. 6664376
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Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Goddard, A.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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Best Local Similarity 99.9
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 118
LENGTH: 1857
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                                                        ; TYPE: DNA
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US-09-905-125A-118
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PAPLICANT: Tunam, Daniel
APPLICANT: Tunam, P. Mickey
APPLICANT: Word, Williams, P. Mickey
APPLICANT: Word, Williams, P. Mickey
APPLICANT: Word, Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic
FILE REPERENCE: 10466-14
CORRENT FILMS DATE: 2001-07-10
FILMS APPLICATION NUMBER: US/09/902,775A
FILMS APPLICATION NUMBER: US/09/414
FRIOR FILMS DATE: 1999-07-26
FRIOR PLING DATE: 1999-07-26
FRIOR FILMS DATE: 1999-07-26
FRIOR PLING DATE: 1999-07-26
FRIOR FILMS DATE: 1999-07-28
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FRIOR FILMS DATE: 1999-07-28
FRIOR FILMS DATE: 1999-09-13
FRIOR FILMS DATE: 1999-09-13
FRIOR FILMS DATE: 1999-09-13
FRIOR FILMS DATE: 1999-11-20
FRIOR FILMS DATE: 1999-11-20
FRIOR PLICATION NUMBER: PCT/US99/28314
FRIOR FILMS DATE: 1999-11-20
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FRIOR FRIINS
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                                                                                                                                                                                                 Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                               Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                   Kljavin, Ivar J.
Mather, Jennie P.
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Matches 1841; Conservative
                                                             Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumas, Daniel
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SEQ ID NO 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-902-775A-118
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                                                             APPLICANT:

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901 AGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCCTGGTGTGAGCCTGGTCG 960
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                                                                                                                    961 GCTCACCGCCTATCATCTGCATTTGCCCTTACTCAGGTGCTACCGGACTCTGGCCCCTGAT
                                                                                                                                                                                                                                                GTCTGTAGTTTCACAGGATGCCTTATTTGTCTTCTACACCCCACAGGGCCCCCTACTTCT
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                                                                     GCTCACCGCCTATCATCTGCATTTGCCTTACTCAGGTGCTACCGGACTCTGGCCCCTGAT
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; Sequence 118, Application US/09902775A
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botsein, David
; APPLICANT: Betsein, David
; APPLICANT: Eaton, Dan L.
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1111 THICCHACACTICATION 1111	RESULT 4 US-09-906-700-118 Sequence 118, Application US/09906700 FARENT NO. 67235108: APPLICANT: Genentech, Inc. APPLICANT: Botstein, David APPLICANT: Botstein, David APPLICANT: Betstein, David APPLICANT: Betstein, David APPLICANT: Perrara, Napoleone APPLICANT: Filvaroff, Ellen APPLICANT: Fong, Shérman APPLICANT: Fong, Wei-Qiang APPLICANT: Gerber, Hanspeter APPLICANT: Gerber, Hanspeter APPLICANT: Godowski, Paul J. APPLICANT: Godowski, Paul J. APPLICANT: Grimaldi, Christopher J. APPLICANT: Manney, Auetin L. APPLICANT: Mather, Jennie P. APPLICANT: Mather, Jennie P.
61 AAGGCGAAGTCGAGAAACTGTTGCCCCTTCATATTGCCGATCCTGTTGTCCCC 120 61 AAGGCGCAAGTCGAGAAACTGTTGCCCTTCATATTGCCGATCCTGTTGTCCC 120 61 AAGGCGCAAGTCGAGAAACTGTTGCCCTTCTAAATTGCGGATCCTGTGGATCCTGTGAATTCTTCTCTGAGAATTCCTGAGAATTCTTCTGAGAATTCTTCTGAGAATTCTTCTGAGAATTCTTCTGAGAATTCTTCTGAGAATTCTTCTGAGAATTCTTCTGAGAATTCTTCTGAGAATTCTTCTTCTAAAATTTCTTCTTGAGAATTCTTCTTCTAAAATTCTTCTTCTAAAATTCTTCTTTTTT	CTTGTAACCCTGATTCTCCTGGGAATCTTGGTTTTTGGCATCTGGTTTGCCTATAGCCGA CTTGTAACCCTGATTCTCCTGGGAATCTTGGTTTTTTGGCATCTGGTTTGCCTATAGCCGA GGCCACTTTGACGAACAAAGAAACGAATCTTGGTTTTTTGGCATCTGGTTTGCCTATAGCCGA GGCCACTTTGACAGAACAAAGAAACGAACTTCGAGTAAGAAGGTGATTTACAGCCGCCT AGTGCCCGAAGTGAAGGAAATCAAACAGACTTCGAGTAACAGAGCTGGTCG AGTGCCCGAAGTGAAGAAAAAAAAACAGACTTCGTGTATCCTGGTGATGACCTGGTCG AGTGCCCGAAGTGAAGGAAATTCAAACAGACTCGTCATTCCTGGTGTGAGCCTGGTCG AGTGCCCGAAGTGAAGAAATTCAAACAGACTCGTCATTCCTGGTGAGCCTGGTCG AGTGCCCGAAGTGAAGAGAATTTGATATTGTCTTCTACACCCCACAGGCCCCCTGAT GTCTGTAGTTTCACAGGATGCCTTATTGTCTTCTACACCCCACAGGGCCCCCTACTTCT GTCTGTAGTTTCACAGGATGCCTTATTGTCTTCTACACCCCACAGGGCCCCCTACTTCT GTCTGTAGTTTCACAGGATGCCTTATTTGTCTTCTACACCCCACAGGGCCCCCTACTTCT TCGGATGTTTTAATAATAATGTCAAGCTATTGTCTTCTACACCCCCACAGGGCCCCCTACTTCT TCGGATGTTTTTAATAATAATGTCAAGCTATTGTCCTCCATCCTCCCCCCCC

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        APPLICANT: Baon, Natholas F.
APPLICANT: Stewart, Timochy A.
APPLICANT: Stewart, Timochy A.
APPLICANT: Stewart, Timochy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wold, William; P. Mickey
APPLICANT: Wold, William; P. Mickey
TITLE OF INVERTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
FILE REPRENCE: 10466-14
CURREWY APPLICATION NUMBER: US/9906,700
CURREWY APPLICATION NUMBER: PCT/US00/0414
PRIOR FILING DATE: 1999-07-07
PRIOR PLICATION NUMBER: PCT/US99/2008
PRIOR PLILING DATE: 1999-07-08
PRIOR PLILING DATE: 1999-01-13
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-20
PRIOR PRIOR PRIICATION NUMBER: PCT/US99/3099
PRIOR PRIOR PLILING DATE: 1999-11-20
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PRIOR APPLICATION NUMBER: PCT/USO0/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 118
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Matches 1841, Conservative
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; ORGANISM: Homo sapiens
US-09-906-700-118
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Score 1840.4;
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
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; ORGANISM: Homo sapiens
US-09-903-603A-118
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Best Local Similarity
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          1321 AGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGACGACCAGGGCCAGCTGT 1380
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APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Screted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: GNE.161822C12
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
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Patent No. 6767995
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
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Eaton, Dan L.
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Sao, Wei-Qiang
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-12-02
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PRIOR PLILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 118
LENGTH: 1857
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Best Local Similarity 99.5
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 118
LENGTH: 1857
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APPLICANT: Thouas, Daniel
APPLICANT: Thouas, Daniel
APPLICANT: Thouas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REPERBENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-00-18
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PRILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-11-30
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                                                                 1801 AGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCA 1842
                                                                                                     FILING DATE: 1999-12-16
APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US99/30999
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Patent No. 6818449
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Rnjavin, Ivar J.
Pan, James
Paoni, Nicholas F.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Stewart, Timothy A.
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APPLICANT: Genemicech, Inc.
APPLICANT: Ashkenazi, Avii
APPLICANT: Botstein, David
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Eaton, Dan L.
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Godowski, Paul J.
Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
             Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Tumas, Daniel
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Paoni, Nicholas F.
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Gerritsen, Mary E.
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Mather, Jennie P.
Botstein, David
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PAPPLICANTY WOOD, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic FILE REFERENCE: 10466-14

CURRENT FILMON. Acids Encoding the Same FILE REFERENCE: 10466-14

CURRENT FILMON MUMBER: US/09/905,381A

PRIOR PELICATION NUMBER: US 60/143,048

PRIOR PELICATION NUMBER: US 60/145,698

PRIOR PELICATION NUMBER: US 60/145,698

PRIOR FILMO DATE: 1999-07-07

PRIOR PELICATION NUMBER: US 60/146,222

PRIOR PELICATION NUMBER: US 60/146,222

PRIOR PELICATION NUMBER: PCT/US99/2094

PRIOR PELICATION NUMBER: PCT/US99/2099

PRIOR PELICATION NUMBER: PCT/US99/2099

PRIOR PELICATION NUMBER: PCT/US99/2091

PRIOR PELICATION NUMBER: PCT/US99/2091

PRIOR PELICATION NUMBER: PCT/US99/2091

PRIOR PELICATION NUMBER: PCT/US99/2091

PRIOR PELICATION NUMBER: PCT/US99/2095

PRIOR PELICATION NUMBER: PCT/US99/2091

PRIOR PELICATION NUMBER: PCT/US99/2099

PRIOR PLINE DATE: 1999-11-30

PRIOR PELICATION NUMBER: PCT/US99/30999

PRIOR PELICATION NUMBER: PC Gaps ö Length 1857; Indels DB 4; ï Score 1840.4; Pred. No. 0; 0; Mismatches 99.9%; ilarity 99.9%; Conservative 0 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-905-381A-118 Query Match Best Local Similarity Matches 1841; Conserv

RESULT 8
3.09-09-05-381A-118
5.8cquence 118, Application US/09905381A
Patent No. 6818746
GENERAL INPORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi

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Pred. No. 0;
0; Mismatches
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Best Local Similarity 99.9%;
Matches 1841; Conservative
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US-09-906-618-118
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APPLICANT: Kornecki, Malgorzata B.
TITLE OF INVENTION: Human Platelet F11 Receptor
FILE REFERENCE: 011.00221
CURRENT APPLICATION NUMBER: US/09/397,243D
CURRENT APPLICATION NUMBER: 60/100,638
PRIOR APPLICATION NUMBER: 60/100,638
PRIOR FILING DATE: 1998-09-16
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
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Matches 1800; Conservative
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ORGANISM: Homo sapiens
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US-09-397-243D-1
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                 CCTGGCTGGCAGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTTCCTTGT
                                            GTACTGACGACCAGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAAT
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOCTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 70
LENGTH: 1421
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Patent No. 6150502
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ORGANISM: Human
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US-09-188-930-70
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                                     ACCATTGGGAACCGGGCAGTGCTGACATGCTCAGAACAAGATGGTTCCCCCACCTTCTGAA
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US-09-188-930-254
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AGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCCTTCTAAGTAGACAGCAAAAA
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                                       AGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCCTTCTAAGTAGACAGCAAAAA
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                                                                                                                                                                                                                                          Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Strachan, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skir;
TITLE OF INVENTION: and Methods for Their Use
TITLE OF INVENTION: 11000.1011c2
CURRENT APPLICATION NUMBER: 1999-05-14
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
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99.3%; Pred. No. 0;
ive 6; Mismatches
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Best Local Similarity 99.3
Matches 1350; Conservative
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; ORGANISM: Mouse
US-09-312-283C-70
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Sequence 254, Application US/09312283C
Patent No. 65731095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Sleeman, Matchew
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.101102
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 254
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Best Local Similarity 99.6%;
Matches 1354; Conservative (
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; ORGANISM: Mouse
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Pred. No. 0;
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APPLICANT: Murison, James Greg; TITLE OF INVENTION: Compositions Isolated Fro; TITLE OF INVENTION: Compositions For Their Use; TITLE REFERENCE: 11000.1011c1 CURRENT APPLICATION NUMBER: US/09/188,930A; CURRENT FILING DATE: 1998-11-09; NUMBER OF SEQ ID NOS: 348; SEQ ID NO 254
LENGTH: 1421
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llarity 99.6%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Human
US-09-188-930-254
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Best Local Simi
Matches 1354;
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FH Key Location/Qualifiers

I. 189442

/ Organism=' Homo sapiens (human)'.
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24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Location/Qualifiers
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Pred. No. 0;
0; Mismatches
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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C12N1/19,
                                                                                                   Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J. Secretory and transmembrane polypeptide and nucleic acid encoding
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                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1842)

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Location/Qualifiers
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0.59139, 118-SEP-1997 US

0.59266, 15-OCT-1997 US

0.62287, 17-OCT-1997 US

0.62814, 24-OCT-1997 US

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0.633145, 24-OCT-1997 US

0.63345, 24-OCT-1997 US

0.63345, 24-OCT-1997 US

0.63345, 28-OCT-1997 US

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0.63544, 28-OCT-1997 US

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0.65186, 17-NOV-1997 US

0.65186, 17-NOV-1997 US

0.65186, 17-NOV-1997 US

0.65611, 24-NOV-1997 US
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Pred. No. 0;
0; Mismatches
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/organism="Homo sapiens"
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                                                                                                                                                         GENENTECH INC
OS Homo sapiens (human)
PN JP 2001516580-A/98
PD 02-OCT-2001
PF 16-SEP-1998 JP 2000511867
PR 17-SEP-1997 US 60/059115
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Homo sapiens (human)
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   AGTGCCCGAAGTGAAGGAGAATTCAAACAGACTCGTCATTCCTGGTGTGAGCCTGGTCG
                                             AGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCCTGGTGTGGGCCTGGTCG
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Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L., Mather, J.P.,
Williams, P.M. and Wood, W.I.
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                                                     GICTGIAGTITCACAGGAIGCCTIATITGICTICTACACCCCACAGGCCCCCTACTICT
                                                                                                        TCGGATGTGTTTTTAATAATGTCGCTATGTGCCCCCATCCTCCTTCATGCCCTCCTCCC
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                                         GTCTGTAGTTTCACAGGATGCCTTATTTGTCTTCTACACCCCACAGGGCCCCCTACTTCT
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Sequence 118 from patent US 6686451.
AR473078.1 GI:42708453
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Patent: US 6686451-A 118 03-FEB-2004;
Location/Qualifiers
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Best Local Similarity 99.9%; Pred. No. 0;
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Sabkenazi, A., Botstein, D., Desnoyers, L., Eaton, D. L., Ferrara, N., Filvaroff, B., Gadowski, F., Gaco, W.-Q., Gerber, H., Gerritsen, M.E., Kljavin, E., Godowski, P. G., Girmaldi, J.C., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Mather, J. P. Pan, J., Panoi, N.F., Roy, M.A., Stewart, T.J., Tumas, D., Williams, P. M. and Wood, W. I.

Secreted and transmembrane polypeptides and nucleic acids encoding the same
Location/Qualifiers

1. 1857

// Organism="unknown"
// mol_type="genomic DNA"
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E 1 (bases 1 to 1857)

RS Bollinger,(L. Jr.

Crane test weight assembly and method

NAL Patent: US 6725730-A 365 27-APR-2004;

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Location/Qualifiers

forganism="unknown"

/mol_type="genomic DNA"
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Pred. No. 0;
0; Mismatches
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US 6725730.
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Best Local Similarity 99.9
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1501 CTCTGCCCTGTCCTCGAATACAAGCTGACATTGACTGTGTGTG	RESULT 15 AX454468 AX454468 AX454468 AX454468.1 G1:21713858 Homo sapiens (human) ORGANISM BUKATYOLE, METAZOA; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens BUKATYOLE, METAZOA; Chordata; Catarrhini; Hominidae; Homo. REFERENCE AUTHORS GOGOWSKI,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W. TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis Genentech, Inc. (US); Baker, Kevin Mary E. (US); Goddard, Autrey (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard, Autrey (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard, Autrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US); Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US); Pan, James (US); Pan, James (US); Pan, James (US); Matanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William	PEATURES 1. 1857 Location/Qualifiers 1. 1857

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C1485 100.6 5.5 464 1 AV720671 AV72071 A	N W	UDURNAL ORDUTISHER DUCKNAL COLLECT: Feng Liang Email: fliang@lifetech.com URL: Http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 REFERENCE 2 (Dases 1 to 1594) AUTHORS Genoscope. TITLE Direct Submission JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage: HTTLE Direct Submission JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr) COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. FEATURES 11594 Author	ORIGIN
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 9100 GENYZ cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
191 9100 GENYZ cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
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/clone="CSOD1055YH06"

/tissue_type="Placenta C
/plasmid="pcMVSPORT_6"
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DB 1084 TCGGATGTGTTTTAATAATGTCAGCTATGTCTCCCTCCCT	1488 bp mRNA linear cbNA clone CS0DI032XK05 of Placenta Ciens (human). GI:50489426 cDNA. g (human) g (human	Query Match 74.2%; Score 1367; DB 3; Length 1488; Best Local Similarity 95.8%; Pred. No. 0;
	ACCATTGGGAACCGGGCAGTGCTGACATGCTCAGAACAGGTGCTCCCCCCCTTCTGAAACCAGGAACCGGGCAGTGCTGACTGCTCAGAACAGAACACAGAACCCGGCAGTGCTTCTGAATGCTCCAAAGCACCCGTGCTTCTTCTTGAACATTCCCAAAGCTGCTCCAAAGCTCCTTCTTTTTTTT	1081 TCGGARGTGTTTTAATAATGTCAGCTATGTGCCCCATCCTCCTTCATGCCCTCCCT

0y 1081 TCGGATGTGTTTTAATAATGTCAGCTAATGTG Db 1068 TCGGATGTGTTTTAATAATGTCAGCTAATGTG 1141 TTTCCTACCACTGCTGATGGCGCAGCAACTTGC 0y 1201 AGGGATCAGGAAGCAATCCTGGGTATGCCATT 1201 AGGGATCAGGAAGCAATCCTGGGTATGCCATT 0y 1261 TGGCGGGGGTCGCAGGAATCCTGGATATGCCATT 0y 1261 TGGCGGGGGTCGCAGGAATCCTGGACTCAACTC 1321 AGGTATCTTCAGCTTGGATTCTGGACTCTCAACTC 0y 1261 TGGCGGGGGTCGCAGGAATCTGGACTCTCAACTC 1321 AGGTATCTTCAGCTTGGATTCTGGACTCTCAACTC 0y 1321 AGGTATCTTCAGCTTGGATTCTGGACTCTAACTC 0y 1321 AGGTATCTTCAGCTTGGATTCTGGACTCTCAACTC 0y 1321 AGGTATCTTCAGCTTGGATCTCGACTCTTCTGT 1322 AGGTATCTTCAGCTTGGAGCTAGAGCGCTCAACTCAACT	FEATURES Location/Qualifiers 1. 1127 Acganism="Homo sapiens" // Organism="Homo sapiens" // Day ref="taxon:9606" // Clone="CSON1055YHO6" // Lissue type="PLACENTA CC / Clone" // Clone Tib="Homo sapiens / Note="Tit strand cDNA wa primer. Five prime end en
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Sequencage
- 91057 EVRY cedex - FRANCE
- 91057 EVRY cedex - FRANCE
h a NotI-oligo(dT) primer. Five prime
NA was digested with Not I and cloned
s of the pCMVSPORT 6 vector. Library
nstructed by Life Technologies, a
equence belongs to sequence cluster
                                                                                                                                              TTGACTTCCCTTCTAAGTAGACAGCAAAA 1260
|||||||||||||||||||||||||||||
TTGACTTCCCTTCTAAGTAGACAGCAAAA 1247
TGCCCCATCCTTCATGCCCTCCCTCCC 1140
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OT 25-NORMALIZED Homo sapiens cDNA
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B PLACENTA COT 25-NORWALIZED"

was primed with a NotI-oligo(dT)

enriched, double-strand cDNA was
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GCTCA-CGCCTATAATCTGCTTTGCCTT 996
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/clone="C80DL004YD03"
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                                                                                 Length 1127;
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                                                                               Score 941.2; DB 1;
Pred. No. 5.2e-232;
7; Mismatches 5;
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al Similarity 98.5%;
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
AL560725 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED HOmo sapiens cDNA clone CSODL004YD03 5-PRIME, mRNA sequence.
AL560725
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1 (200 Sess 1 to 9 Sessee, J. and Polayes, D.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
On Feb 15, 2001 this sequence version replaced gi:31284854.
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/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CSODL004CB02QPl&c=250.r.
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;; Pred. No. 2.1e-231;
12; Mismatches 9;
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/mol_type="mRNA"
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/organism="Homo sapiens"
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                    For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0DI075DF12NP1&c=250.r. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             Length 1084;
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AL576433 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI075YL24 3-PRIME, mRNA sequence.

AL576433.3 GI:46249298
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequeré@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSFORT 6 vector. Library
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Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization (brobblished (2001)
On Peb 16, 2001 this sequence version replaced gi:31314719.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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Full-length cDNA libraries and normalization
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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Contact: Genoscope
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1; Mismatches 19;
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/mol_type="mRNA"
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E 1 (Bases I to 886)

I (Bases I to 886)

I Unpublished (1999)

L Ontolished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2660 row: k column: 24

High quality sequence stop; 698.
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5/, mRNA sequence.
     547 TACACCTGGTTCAAAGATGGGATAGTGATGCCTACTAATCCCAAAAGCACCCGTGCCTTC 606
                                                            607 AGCAACTCTTCCTATGTCCTGAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCTGTCA
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                                                                                                                                                                                                                                                                                                                         /tissue_type="carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NHH_MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site_1: Xho1;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into BcoRI/AhoI sites using the
following 5' adaptor: GGCACCAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
C California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6481188"
                Contact: Robert Strausberg, P
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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BM548873.1 GI:18783816
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  Length 886;
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 tch 46.7%; Score 859.6; DB 5; al Similarity 99.4%; Pred. No. 6.4e-211; 862; Conservative 0; Mismatches 5;
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                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                            Amammatical buttlerial Filmates) Catafillini, Hominidae; Homo.

S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM12756 row: m column: 22
High quality sequence stop: 666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_88"
/note="lorgan: small intestine; Vector: pCMV-SPORT6;
Site_l: Notl; Site_2: Sall; Cloned unidirectionally;
Oligo-dT primed. Average insert size 1:76; kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5740989"
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Matches 857; Conservative
Homo sapiens
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BX372242 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-APR-2004 BX372242 Homo sapiens CODC004YD03 3-PRIME, mRNA sequence.
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                                     GECTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGAACA
                                                                                                                                                                                              CTGGCATTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAAT
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                   GTCTGTTCCCAGGAGTCCTTCGCGGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGACA
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                                                                                                                                                                        CTGGCATTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAAT
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CE 1 (bases 1 to 896)

LiyuB., Gruber.C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization

Unpublished (2001)

On May 8, 2003 this sequence version replaced gi:30456760.

Contact: Genoscope
Contact: Genoscope.

Contact: Genoscope. On the sequence of the Sequence of the Sequence of the Sequence of Genoscope.

In Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: sequence contact.

Is sequence DNA was primed with a NotI-oligo dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a davision of Invitrogen. This sequence belongs to sequence cluster
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//cissue Vtye="PIACBNTA COT 25-NORWALIZED"
//clone lib="Homo sapiens PIACENTA COT 25-NORWALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                       CGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACAACAG
AACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGATGGGATAGTGATGCCTA
                                   CGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACAACAG
                                                                                                              GAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACAGCTGTGAGGCAC
                                                                                                                                  GGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGA
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Pred. No. 1.4e-206;
1; Mismatches 3;
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                       GTAAGAAGGTGATTTACAGCCAGCC 899
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Best Local Similarity 99.5%;
Matches 844; Conservative 1
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Genosocpe - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequefe@Genoscope.cns.fr, Web : www.genoscope.cns.fr restrand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                             GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTC 1238
                                                                                                                                                                                                                                                                                                                  CCTTCTAAGTAGACAGCAAAAATGGCGGGGGTCGCAGGAATCTGCACTCAACTGCCCACC 1298
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AL549598 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CS0DI055YH06 3-PRIME, mRNA sequence.
       CCCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCCAT 1118
                                                                                                                                                                                                                                                               237 GIGTTTATTCCCCATTTCTTTGAGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTC 178
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/db_xrefe=texcn:9606"
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/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens primed with a NotI-oligo (dT)
/primer="Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                          CCTCCTTCATGCCCTCCCTCTCCTACCACTGCTGAGTGGCCTGGAACTTGTTTAAA
                                                                                                                                       CCTCCTTCATGCCCTCCCTCTCCTATCCTACCACTGCTGAGTGGCCTGGAACTTGTTTAAA
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                                     CCCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTTAATAATGTCAGCTATGTGCCCCAT
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31271416.
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catarrhini; Hominidae; Homo
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94.0%; Pred. No. 2.3e-203;
tive 13; Mismatches 37;
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Mammalia; Eutheria; Primates;
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                                                                                                                                                  Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr. Web : www.genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the NotI and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol type="mRNA"
/db Zref="taxon:9606"
/clone="CSOBLOGYTOG"
/cell type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/cell line="RAMOS CELL LINE"
/clone lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 907)
1 (Ja. M. Gruber, C., Jessee, J. and Polayes, D.
Full-length cDMA libraries and normalization
Unpublished (2001)
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0; Mismatches 23;
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al Similarity 97.2%;
872; Conservative
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Best Local S:
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                                                 -AATCCCMAAGGCACCCGTGCHTAAAAAAWMTTCCTATGTCCTAAATCCCACNAACAG
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BX327155 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI032XC02 5-PRIME, mRNA sequence.

RESULT 14 BX327155 LOCUS DEFINITION

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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Genoscope - Centre Centre S. 2 rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Ist strand cDNA was primed with a Not1-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Ecok V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAF0242F12_AF02303_2&c=250.r.
Location/Qualifiers
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/tissue type="PLACENYA COT 25-NORMALIZED"
/tissue type="PLACENYA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENYA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Pull-length cDNA libraries and normalization
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B I (bases 1 to 907)

S NIH-MCC http://mgc.nci.nih.gov/.

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-romail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://mage.llnl.gov

Plate: LLCM2660 rowv

Llocation/Qualifiers
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Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                            1;
                                                                                                                                               907;
                                                                                                                                             Length
                                                                                                                                                                                            Indels
                                                                                                                                        Score 803.2; DB 5;
Pred. No. 2.5e-196;
); Mismatches 13;
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                                                                                                                                             43.6%;
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8, 2005, 13:22:01

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Length 1857;

DB 3;

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DB 3;

DB 3; Length 1857;

Length 1857;

DB 4;

DB 4; Length 1857;

DB 4; Length 1857;

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Human cDNA clone DNA40628-1216 encoding PRO301 (UNQ264) WO200119991-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC97460 standard; cDNA; 1857 BP.
Human angiogenesis-associated protein PRO301 cDNA, SEQ
WO200053753-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           мьы уэрвү standard; cDNA; 1857 BP.
Human anglogenesis related cDNA PRO301 SEQ ID NO: 53.
WO200208284-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS21426 standard; cDNA; 1857 BP.
Human cDNA sequence encoding for PRO301 polypeptide
WO200140466-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of human polypeptide PRO301. M2200077037-A2. Carmer 2000.
                Score 1840.4;
Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Human PRO301 cDNA sequence SEQ ID NO:53.
WO200200690-A2.
                                                                                        AAA49723 standard; cDNA; 1857 BP.
Human PRO301 cDNA clone DNA40628-1216.
WC200037638-A2.
29-UDN-2000.
                                                                                                                                                                                                                                                                                              ADC78438 standard; cDNA; 1857 BP.
Human PRO301 cDNA.
WO200015796-A2.
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Human PRO301 cDNA.
WO200104311-A1.
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99.9%; S.
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(B-747 ) GENENTECH INC. 99.9%;
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(GETH ) GENENTECH INC.
12Y Match 99.9%;
it Local Similarity 99.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                  Best Local Similarity RESULT 6
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(GETH ) GENI
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RESULT 13
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RESULT 8
GenCore version 5.1.6
September 8, 2005, 10:59:16; Search time 1032 Seconds (without alignments)
10566.050 Million cell updates/sec
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                                                                                                                                                                Sequence:

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0
Searched:

Searched: 4390206 seqs. 2559870667 residues
Total number of hits satisfying chosen parameters: 8780412
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Human secreted/transmembrane protein cDNA, #25.
US2004137561-A1.
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(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
99.9%; Pred. No. 0;
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Best Local Similarity 99.9%; Pred. No. 0;
RESULT.4
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Human PRO301 protein encoding cDNA, UNQ264.
WO200015797-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1840.4;
Pred. No. 0;
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Human cDNA clone DNA40628 encoding PRO301
WO9914241-A2.
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Maximum Match 100%
Listing first 1500 summaries
Database : N_Geneseq_16Dec04;*
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Protein PRO301 cDNA clone DNA40628-1216.
WO9914328-A2.
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Human PR0301 cDNA sequence SEQ ID NO:89.
WO20003221-A2.
08-JUN-2000.
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25-MAR-1999.
(GETH ) GENENTECH INC.
99.94;
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1842
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Maximum DB seq length: 200000000
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 2
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Best Local Similarity
RESULT 3
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RESULT
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Length 1857;

DB 4;

DB 6; Length 1857;

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Score 1840.4; DB 6; Length 1857; Pred. No. 0;
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DNA encoding novel secreted and transmembrane protein PRO301 US2003017563-A1.
                                                                                                                                                                                                                                                                                                          ACD07497 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2002197671-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003032063-A1.
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Whumn cDNA encoding secreted/transmembrane protein PRO301.
US2002132240-A1.
19-SEP-2002.
                                                                                                                                                                                                                      Human cDNA for secreted/transmembrane protein PRO301.
US2003003530-A1.
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Human secreted/transmembrane polypeptide PRO301 cDNA.
US2003044839-A1.
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26-DEC-2002.
(GETH ) GENENTECH INC.
(BLTH ) GENENTECH INC.
18ry Match 99.9%; Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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cDNA encoding human PRO polypeptide #183.
20.FEB-2003.
(GETH ) GENENTECH INC.
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) GENENTECH INC.
99.9%; Sr
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02-JAN-2003.
(GETH ) GENENTECH INC.
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                           (GDDD) CODDARD A.
(GDDD) CODDWSKI P J.
(GTRN) GURNEY A L.
(HILL) HILLIAN K J.
(MARS) MARSTERS S A.
(PANJ) PAN J.
(STEP) STEPHAN J.
(STEP) STEPHAN J.
(WTLL) WILLIAMS P M.
          GERBER H.
GERRITSEN M E.
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21H ) GENENTECH 1.

21Y MATCH
Best Local Similarity >> RESULT 18
ID ABX71545 stand**
DE Human CDNA
PN US20021**
PD 19-**
PA
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Best Local Similarity
RESULT 21
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Best Local Similarity
RESULT 16
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RESULT 22
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Human cDNA encoding a secreted/transmembrane protein, SEQ ID 365.
US2003032155-A1.
13-FEB-2003.
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Pred. No. 0;
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                                                                           8; Length 1857;
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Novel human secreted and transmembrane protein PRO301 CDNA, 2200217165-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003017463-A1.
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Novel human secreted and transmembrane protein PRO301 DNA US2003032062-A1.
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Human cDNA encoding secreted/transmembrane protein PRO301
US2003032057-A1.
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Human secreted / transmembrane polypeptide PRO301 cDNA
US2003036060-A1.
ACD41977 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein (PRO) cDNA #183.
US2003036179-A1.
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                                   US&volutions
20-FB-2003.
(GETH) GENENTECH INC.
GETH) GENENTECH INC.
99.9%; Score 1840.4;
ery Match 99.9%; Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Human secreted/transmembrane protein cDNA,
US2002160374-A1.
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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31-OCT-2002.
(GETH ) GENENTECH INC.
99.9%;
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28-NOV-2002.
(GETH ) GENENTECH INC.
99.9%;
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13-FBD-2003.
(GETH ) GENENTECH INC.
MALCh '1-rity 99.9%;
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30-JAN-2003.
(GETH ) GENENTECH INC.
Match 'Trity 99.9%;
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(GETH ) GENENTECH INC.
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23-0AN-2003.
(GETH ) GENENTECH INC.
99.9%;
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Best Local Similarity
RESULT 26
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RESULT 27
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Length 1857;
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(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003082693-Al.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003087345-A1.
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Human CDNA encoding secreted/transmembrane protein PRO301.
052003045693-A1.
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US2003039971-A1.
27-FEB-2003.
(GETH ) GENENTECH INC. 99.9%; Score 1840.4; DB
st_Local Similarity 99.9%; Pred. No. 0;
                  08-MAY-2003.
(GETH ) GENENTECH INC.
Query Match 99.9%; Score 1840.4;
Best Local Similarity 99.9%; Pred. No. 0;
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Pred. No. 0;
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cDNA encoding human PRO polypeptide #183.
US2003068794-A1.
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US2003068795-A1.
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Human PRO polynucleotide #183.
US2003082763-A1.
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Human PRO polynucleotide #183
US2003073215-A1.
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06-MAR-2003.
(GETH ) GENENTECH INC.
Match 'Trity 99.9%;
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10-ARP-2003.
(GETH) GENENTECH INC.
GETH) 99.9%;
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PA (GETH ) GENENTECH INC.
Query Match 99.9%;
Best Local Similarity 99.9%;
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 44
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     US2003087350-A1.
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PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1840.4; DB 9; Length 1857;
RESULT 33
                                                                    Length 1857;
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(GETH ) GENENTECH INC.
ery Match 99.9%; Score 1840.4; DB 9; Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003022328-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003068796-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003082711-A1.
Human secreted / transmembrane polypeptide PRO301 cDNA.
US2003027143-A1.
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(GETH ) GENENTECH INC.
17 Match 99.9%; Score 1840.4;
27 Match 99.9%; Pred. No. 0;
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13-MAR-2003.
(GETH ) GENENTECH INC.
PARY MAICh 99.9%; Score 1840.4;
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01-MAY-2003.

(GETH ) GENENTECH INC.

99.9%; Score 1840.4;

1017 Match 99.9%; Pred. No. 0;
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Pred. No. 0;
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Human secreted/transmembrane protein cDNA,
US2003092002-A1.
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cDNA encoding human PRO polypeptide #183.
US2003082704-A1.
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Human PRO polynucleotide #183.
US2003073212-A1.
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Human PRO polynucleotide #183.
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             US20050...
17-APR-2003.
(GETH ) GENENTECH INC.
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                                                            Query Match
Best Local Similarity
RESULT 32
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Best Local Similarity
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US2003049816-A1.
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RESULT 40 ID ADB15 DE Human

RESULT 38

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RESULT 37

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RESULT 39

DB 9; Length 1857;

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99.9%; Score 1840.4; 99.9%; Pred. No. 0;
                                                                  ADB13237 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003082710-A1.
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            (GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 612000
ID ADA74491 standard; cl
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PN US2003068798-A1.
PD 10-ARR-2003.
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RESULT 59
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RESULT 60
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RESULT 62
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RESULT 64
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                                          DB 9; Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003073211-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA. US2003082691-A1.
01-MAY-2003.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003082694-A1.
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08-MAY-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
ery Match 99.9%; Pred. No. 0;
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(GETH ) GENENTECH INC.
2ry Match 99.9%; Score 1840.4;
2ry Match 99.9%; Pred. No. 0;
                                                                                  ADB16698 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003087349-A1.
08-MAY-2003.
GETH ) GENENTECH INC.
99.9%; Score 1840.4;
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24-APR-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
ery Match
99.9%; Pred. No. 0;
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Pred. No. 0;
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Human secreted/transmembrane protein cDNA,
US2003049621-A1.
                                                                                                                                                                                               Human PRO polymucleotide #21. US2003044793-A1.
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Human PRO polynucleotide #183.
US2003077722-A1.
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Human PRO polynucleotide #183.
US2003087351-Al.
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Best Local Similarity 9
RESULT 54
ID ADB14853 stand>
DE Human PRO r
PD US2030r
PA
                                      Query Match
Best Local Similarity 9
RESULT 50
ID ADB16698 standard; CDN
DE Human PRO polynucleoti
PN US20033087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity 9
BESULT 58
ID ADB19925 standard; CDN
DE Novel human secreted a
PN US2003082691-A1.
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Best Local Similarity
RESULT 57
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RESULT 55
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Best Local Similarity
RESULT 56
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10-AFK-2005.
(GETH ) GENENTECH INC.
pry Match 99.9%; Score 1840.4; DB 9; Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003082708-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003082695-Al.
                                                                                                  ACD96606 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA US2003044945-A1.
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Human secreted/transmembrane protein cDNA, #25.
US2003054401-A1.
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(GETH ) GENENTECH INC.
(GETY Match 99.9%; Score 1840.4;
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(GETH ) GENENTECH INC.
17 Match 99.9%; Score 1840.4;
17 Match 99.9%; Pred. No. 0;
                                               Score 1840.4;
Pred. No. 0;
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Pred. No. 0;
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Human PRO polynucleotide SEQ ID NO 365.
US2003077713-A1.
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17.APR-2003.
GETH J GENENTECH INC.
Dury Match
Best Local Similarity 99.9%; Score
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Human PRO polynucleotide #183.
102003068798-Al.
USZUCZCZ
01-MAY-2003.
(GETH ) GENENTECH INC.
MATCh '''THIEV 99.9%;
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22-MAY-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4; DB 9; Length 1857;
99.9%; Score 1840.4; DB 9; Length 1857; 99.9%; Pred. No. 0;
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                                                    ACD23226 standard; cDNA; 1857 BP.
Human PRO polynucleotide #21.
US2003064367-A1.
03-APR-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4; st Local Similarity 99.9%; Pred. No. 0;
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24-APR-2003.
(GETH ) GENENTECH INC.
PST MATCh 99.9%; Score 1840.4;
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                                                                                                                                                                                                                                                                                                         99.9%; Score 1840.4; 99.9%; Pred. No. 0;
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CDNA encoding human PRO polypeptide #183.
US2003073214-A1.
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cDNA encoding human PRO polypeptide #183.
US2003092147-A1.
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cDNA encoding human PRO polypeptide #183.
US2003096386-A1.
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Human PRO polynucleotide SEQ ID NO 365.
US2003077715-A1.
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Human PRO polynucleotide #183.
US2003082761-A1.
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Human PRO polynucleotide #183.
US2003082703-A1.
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Human PRO polynucleotide #183.
US2003073210-A1.
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Human PRO polynucleotide #183.
US2003077721-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 70
ID ADA80521 standard; CDN
DE Human PRO polynucleoti
PN US2003082761-A1.
PP O I-MAY-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 75
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RESULT 69
                Best Local Similarity RESULT 68
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DB 9; Length 1857;
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Novel human secreted and transmembrane protein PRO301 CDNA.
                                                                             USZUCZO.
13-MAR-2003.
(GETH ) GENENTECH INC.
ery Match 99.9%; Score 1840.4;
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PA (GETH ) GENENTECH INC.
Query Match 99.9%; Score 1840.4;
Best Local Similarity 99.9%; Pred. No. 0;
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(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
gry Match 99.9%; Pred. No. 0;
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(GETH) GENENTECH INC.
Query Match
99.9%; Score 1840.4;
Best Local Similarity 99.9%; Pred. No. 0;
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Best Local Similarity 99.9%; Pred. No. 0;
RESULT 85
 99.9%; Pred. No. 0;
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US2003082760-A1.
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cDNA encoding human PRO polypeptide #183.
US2003077710-A1.
                                                                                                                                                                                ADB24172 standard; cDNA; 1857 BP.
Human PRO polynucleotide SEQ ID NO 365.
US2003077714-Al.
                                                                                                                                                                                                                                                                                                                                    ADA96501 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003082690-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA81073 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003082702-A1.
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Human PRO polynucleotide #183.
US2003082759-A1.
                                    ADA61025 standard; cDNA; 1857 BP
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US2003068797-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
Query Match
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RESULT 82
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Best Local Similarity
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                                                      Homo sapiens.
US2003049817-A1.
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Length 1857;
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            ADA86945 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003082709-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA46436 standard; cDNA; 1857 BP.

Novel human secreted and transmembrane protein PRO301 cDNA.

V USZ003054516-A1.

20-MAR-2003.

A (GBTH ) GENENTECH INC.

99.9%; Score 1840.4; DB 9; Length 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APA88048 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003082700-A1.
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                                                                                                                                                                 #25.
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                                                                                                                                                                                                                                                                                                   Human secreted/transmembrane protein cDNA, #25.
US2003049622-A1.
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DE Novel human secreted and transmembrane prote PD US203082700-A1.
PD U-MAY-2003.
PA (GETH ) GENENTECH TANC
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Best Local Similarity 99.9%; Pred. No. 0;
RESULT 94
                                                                                                                                                               Human secreted/transmembrane protein cDNA, US2003039969-A1.
                                                                                                                                                                                                                                  Score 1840.4;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 89
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Best Local Similarity 99.9%; Pred. No. 0;
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Pred. No. 0;
                                                                                            99.9%; Score 1840.4; 99.9%; Pred. No. 0;
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Human secreted/transmembrane protein cDNA,
US2003017498-A1.
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cDNA encoding human PRO polypeptide #183.
US2003082699-A1.
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                                                                                                                                               ADA16578 standard; cDNA; 1857 BP
                                                                                                                                                                                                                       Best Local Similarity 99.9%; Sc
RESULT 88
ID ADAJ3007 standard; CDNA; 1857 BE
DE Human secreted/transmembrane pro
PN US2003049652-A1.
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(GETH ) GENENTECH INC.
99.9%;
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JS-A1.
JAH ) GENENTECH IN
JETY MATCh
Best Local Similarity 9
RESULT 87
ID ADA16578 standa-
DE Human secre-
PN US2034-
PA 27-7
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 93
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Best Local S
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ID ADA46
DE Novel
PN US200
PD 20-MP
RESULT 86
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10-APR-2003.
(GETH) GENENTECH INC.
ery Match 99.9%; Score 1840.4; DB 9; Length 1857;
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ADB29018 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003082706-Al.
01-MAY-2003.
(GETH ) GENENTECH INC.
195 Match
196 Match
197 99.9$; Score 1840.4; St Local Similarity 99.9$; pred. No. 0;
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Best Local Similarity 99.9%; Pred. No. 0;
RESULT 98
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(GETH ) GENENTECH INC.
(ery Match 99.9%; Score 1840.4;
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US2003022239-A1.
                                                                                                                                                                                                                                Human PRO polynucleotide #183.
022003059909-Al.
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DA66986 standard; cDNA; 1857 BP.
Human PRO polynuclectide #183.
US2003068793-A1.
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Human PRO polynucleotide
US2003064923-Al.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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.usTH ) GENENTECH 1
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Best Local Similarity 2
RESULT 103
ID ADA66986 stand2
DE Human PRO 7
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PD 10
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RESULT 99 call Similarity
ID ADB27362 standard; cl
DE CDNA encoding human PN US200302229-A1.
PD 30-JAN-2003.
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                                                                                                                                                                                     Best Local Similarity RESULT 96
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01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                           Best Local Similarity RESULT 114
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RESULT 118
                                                                                                                                                            Local Similarity
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Best Local Similarity
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                                                                                                                                                                                        ADA92342 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA, 01.2003082112-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003082766-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003087347-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003082689-A1.
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                                DB 9;
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Human secreted/transmembrane protein cDNA, #25.
US2003077654-A1.
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(GETH ) GENENTECH INC.
ry Match 99.9%; Score 1840.4;
ry Match 99.9%; Pred. No. 0;
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(GETH ) GENENTECH INC.

99.9%; Score 1840.4;

99.9%; Pred. No. 0;
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(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
ery Match 99.9%; Pred. No. 0;
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                               Score 1840.4;
Pred. No. 0;
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Pred. No. 0;
                                                                          ADB23620 standard; cDNA; 1857 BP.
Human PRO polymucleotide SEQ ID NO 365.
US2003077712-A1.
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Human PRO polynucleotide #183.
US2003082698-A1.
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Human PRO polynucleotide #183.
US2003082762-A1.
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US2003087352-A1.
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01-MAY-2003.
(GETH ) GENENTECH INC:
MATCh 'Twity 99.9%;
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Best Local Similarity 99.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 108
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Best Local Similarity
RESULT 109
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RESULT 112
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RESULT 107
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RESULT 113
24-APR-2003
(GETH ) GEN
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Length 1857;
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     DB 10; Length 1857;
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                                                   ADB39490 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA
US2003082764-A1.
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Novel human secreted and transmembrane protein PRO301 CDNA
012003082687-A1.
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Human secreted/transmembrane protein cDNA, #25
US2003082542-A1.
   Score 1840.4;
Pred. No. 0;
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(GETH ) GENENTECH INC.
P9.9%; Score 1840.4;
erv Match 99.9%; Pred. No. 0;
                                                                                                                                     Score 1840.4;
Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Human PRO polynucleotide SEQ ID NO 365.
US2003077717-A1.
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Human PRO polynucleotide SEQ ID NO 365.
US2003077716-A1.
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Human PRO polynuclectide SEQ ID NO 365.
US2003077718-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB86720 standard; cDNA; 1857 BP.
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) GENENTECH INC.
99.9%; Sr
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US2003082697-A1.
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24-APR-2003.
(GETH ) GENENTECH INC.
99.9%; /
99.98;
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01-MPY-2003.
(GETH ) GENENTECH INC.
99.9%;
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Local Similarity 99.9%;
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(GETH ) GENENTECH INC.
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13-MAR-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4; DB 10; Length 1857;
   DB 10; Length 1857;
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                                                                                                                                                           ADB46533 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003082692-A1.
                                                                                                                    DB 10;
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Human secreted/transmembrane protein cDNA, #25.
US2003059828-Al.
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   Score 1840.4;
Pred. No. 0;
                                                                                                                  1840.4;
No. 0;
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Pred. No. 0;
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Human secreted/transmembrane protein cDNA,
US2003059772-A1.
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Pred. No. 0;
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Pred. No. 0;
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Human secreted/transmembrane protein cDNA,
US2003036094-A1.
30-FEB-2003.
(GETH ) GENENTECH INC.
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Pred. No. 0;
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Pred. No. 0;
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Human secreted/transmembrane protein cDNA,
US2003059829-A1.
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Human secreted/transmembrane protein cDNA,
US2003036061-A1.
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Pred. No. 0;
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                                        ADB36138 standard; CDNA; 1857 BP.
Human PRO polynucleotide SEQ ID NO 365.
US2003077720-A1.
                                                                                                                    Score
Pred.
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                                                                       US20030.
24-ARY-2003.
(GETH ) GENENTECH INC.
99.9%;
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PA (GETH ) GENENTECH INC.
QUery March
Best Local Similarity 99.9%;
RESULT 125
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 129
ID ADC34264 standard; CD
DE Human secreted/transm
PN USZ003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Ouery Match
Rest Local Similarity
RESULT 123
ID ADB36138 standard; cf
DE Human PRO polynucleot
PD 24-ARR-2003.
PA (GETH ) GENENTECH INC
                                                                                                                  Query Match
Best Local Similarity
RESULT 124
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Best Local Similarity
RESULT 131
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Best Local Similarity
RESULT 128
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Length 1857;
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Novel human secreted and transmembrane protein cDNA Seq ID365.
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Novel human secreted and transmembrane protein cDNA Seq ID365.
US2003087365-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003092106-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003092107-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003092105-A1.
                                                       Human secreted/transmembrane protein cDNA, #25.
US2003054400-A1.
CBCT-MAR-2003.
(GETH) GENENTECH INC.
199.9%; Score 1840.4; DB 10; St Local Similarity 99.9%; Pred. No. 0;
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US2003054441-A1.
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15-MAY-2003.
(GFTH ) GENENTECH INC.
1ery Match 99.9%; Score 1840.4;
? ^*milarity 99.9%; Pred. No. 0;
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17-APR-2003.
(GETH) GENENTECH INC.
18-ry Match 99.9%; Score 1840.4;
99.9%; Pred. No. 0;
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No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Best Local Similarity 99.9%; Pred. No. 0;
RESULT 132
ID ADC12910 standard; CDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA,
PN US2003073079-A1.
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Best Local Similarity 99.9%; Pred. No. 0; RESULT 132
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Pred.
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                                          CDNA; 1857 BP
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20-MRR-2003.
(GETH ) GENENTECH INC.
Match '1-rity 99.9%;
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15-WAY-2003.
(GETH ) GENENTECH INC.
99.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 133
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RESULT 139
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Best Local Similarity
                                       ADC40735 standard;
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RESULT 138
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Length 1857;

DB 10;

Length 1857;

DB 10;

DB 10; Length 1857;

Length 1857;

DB 10;

Length 1857;

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Length 1857;

DB 10;

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us-10-785-220b-11.rng.spdi

RESULT 141

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ADD03190 standard; cDNA; 1857 BP. Novel human secreted and transmembrane protein PRO301 cDNA. US20033092104-A1. 15-VAY-2003. (GETH ) GENENTECH INC.
                                                                                                                                 AUC90182 standard; CDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 CDNA.
US2003087348-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD04594 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA
US2003087354-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC80550 standard, cDNA, 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA US2003092103-A1.
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Human secreted/transmembrane PRO polypeptide cDNA #27.
US2003105011-A1.
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Pred. No. 0;
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16-0CT-2003.

(GETH ) GENENTECH INC.

99.9%; Score 1840.4;

99.9%; Pred. No. 0;
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Query Match
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 153
                                                                                          Score 1840.4;
Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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CDNA encoding human PRO polypeptide #183.
US2003194770-A1.
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US2003194773-A1.
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Human PRO polynucleotide #183.
US2003194776-A1.
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Human PRO polynucleotide #183.
US2003194774-A1.
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2003.
) GENENTECH INC.
99.98; Sr
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08-MAY-2003.

(GETH ) GENENTECH INC.

MATCh 'lavity 99.9%;
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35-2003.
(GETH ) GENENTECH INC.
99.9%;
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Local Similarity 99.9%;
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(GETH ) GENENTECH INC.
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RESULT 155
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RESULT 154
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RESULT 159
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ADC48490 standard;
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                                                                   08-WAY-2003.
(GETH) GENENTECH INC.
ETY MATCh
-- Tomal Similarity 99.9%; Score 1840.4; DB 10; Length 1857;
                                                                                                                                                                                                                             OB-TMAI-2005.
(GETH) GENENTECH INC.
PLY MATCH 99.9%; SCORE 1840.4; DB 10; Length 1857; Tronal Similarity 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 1857;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1840.4; DB 10; Length 1857; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.9%; Score 1840.4; DB 10; Length 1857; 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1857;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC53545 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein cDNA Seq ID365.
US2003087364-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC54584 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein cDNA Seg ID365.
US2003087363-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC59068 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein cDNA Seq ID365.
US2003087359-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC55946 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein cDNA Seq ID365.
US2003087360-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADCS8516 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein cDNA Seq ID365.
US2003087346-Al.
                 ADC60484 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003087367-A1.
                                                                                                                                                              ADC50959 standard; cDNA; 1857 BP.

Wovel human secreted and transmembrane protein PRO301 cDNA, US2003087361-A1.
08-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted/transmembrane protein cDNA, #25.
US2003082541-A1.
                                                                                                                                                                                                                                                                                                                                                                      08-MAY-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
ery Match 99.9%; Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                ADC65486 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. US2003087362-A1. 08-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC12362 standard; cDNA; 1857 BP.
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18-MAY-2003.
(GETH) GENENTECH INC.
99.9%;
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PA (GETH ) GENENTECH INC.
QUETY MATCh 99.9%;
Best Local Similarity 99.9%;
RESULT 150
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                       Best Local Similarity
RESULT 142
                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 143
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Best Local Similarity
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RESULT 145

RESULT 146

BEREE

DB 10; Length 1857;

Length 1857;

DB 10;

RESULT

Length 1857;

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US2003194792-A1.
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Human secreted/transmembrane protein cDNA, #25.

Human secreted/transmembrane protein cDNA, #25.

US2003104381-A1.

OS-JUN-2003.

(GETH ) GENEWTECH INC.

99.9%; Score 1840.4; DB 10; Length 1857;

St Local Similarity 99.9%; Pred. No. 0;
                                                                                                                                                          99.9%; Score 1840.4; DB 10; Length 1857; 99.9%; Pred. No. 0;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003087358-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD11302 standard; cDNA; 1857 BP.
Human secreted/transmembrane PRO polypeptide cDNA #27.
20203105103-A1.
05-JUN-2003.
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16-00T-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
ery Match 99.9%; Pred. No. 0;
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1840.4;
Pred. No. 0;
                                                                                                                                                                                                                                                                               ADD04917 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA,
US2003104469-A1.
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Human secreted/transmembrane protein cDNA, US2003108983-A1.
12-JUN-2003.
(GETH ) GENENTECH INC.
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Human PRO polynucleotide #183.
US2003194775-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD52319 standard; cDNA; 1857 BP.
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) GENENTECH INC.
99.9%; F
Human PRO polynucleotide #183.
US200319471.Al.
16-OCT-2003.
(GETH ) GENENTECH INC.
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Best Local Similarity 9
RESULT 165
ID ADD03499 standard; cDN
DE Human secreted/transme
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
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LOS MATCH GENENTECH LY

Best Local Similarity RESULT 166

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Best Local Similarity
RESULT 168
ID ADD53059 standard; ci
DE CDNA encoding human i
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Best Local Similarity
RESULT 164
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Length 1857;
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                                Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA. US2003203432-A1.
                                                                                   ADD53611 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003203437-A1.
                                                                                                                                                                                                                                           #27
                                99.9%; Score 1840.4; DB 10; 99.9%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                        ADD37095 standard; cDNA; 1857 BP.
Human secreted/transmembrane PRO polypeptide cDNA
US2003105012-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
FIY Match 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 99.9%; Score 1840.4; Local Similarity 99.9%; Pred. No. 0;
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30-CCT-2003.
(GETH ) GENENTECH INC.
16rV Match 99.9%; Score 1840.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1840.4;
Pred. No. 0;
                                                                                                                                                                        Score 1840.4;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                             Score 1840.4;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                              ADD51767 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003194779-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD02000 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003203430-A1.
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Human PRO polynucleotide #183.
US2003203431-A1.
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Human PRO polynucleotide #183.
US2003199055-A1.
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Human PRO polynucleotide #183.
US2003199057-A1.
                                                                                                                   US2003202.
30-0CT-2003.
(GETH ) GENENTECH INC.
21-Ch ....th ....th 99.9%;
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30-001-2003.
(GETH ) GENENTECH INC.
MAECh '...tV 99.9%;
                                                                                                                                                                                                                                                                                                             99.98;
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(GETH ) GENENTECH INC.
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16-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                             05-JUN-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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...c.TH ) GENENTECH 1
...dery Match
Best Local Similarity >> RESULT 175
ID ADD92499 stand>> DE Human PRO r
PN US2003'
PD 23-'
PA
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                                                                                                                                                                                    Best Local Similarity RESULT 170
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
RESULT 171
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RESULT 176
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RESULT 174
                                           Best Local Similarity RESULT 169
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PA (GETH ) GENENTECH INC.

Query Match

99.9%; Score 1840.4; DB 10;

Best Local Similarity 99.9%; Pred. No. 0;

RESULT 187
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ID ADD78908 standard, CDNA, 1857 BP. DE CDNA encoding human PRO polypeptide PN US2003203429-A1.

PD 30-OCT-2003.

PA (GETH ) GENENTECH INC
                                                                             ADD93051 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. US2003194768-A1.
                                                                                                                                                                                                                               ADE19471 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. U3-002199025-A1. C3-007-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA; 1857 BP.
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US2003199059-A1.
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US2003199026-A1.
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US2003199033-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 191
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RESULT 195
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Best Local Similarity
RESULT 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE18919 standard;
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Human PRO polynucleotide #183.

105203199053-A1.

23-OCT-2003.

(GETH ) GENENTECH INC.

99.9%; Score 1840.4; DB 10; Length 1857; st Local Similarity 99.9%; Pred. No. 0;
                                         Length 1857;
                                                                                                                                                                                            99.9%; Score 1840.4; DB 10; Length 1857; 99.9%; Pred. No. 0;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003194767-A1.
                                                                                           ADE32306 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003194765-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE33962 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003194791-A1.
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                                         DB 10;
                             Query Match
Best Local Similarity 99.9%; Score 1840.4;
RESULT 178
ESCH 178
DE Novel human secreted and transmembrane prott
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
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30-007-2003,
GETH ) GENENTECH INC.
99.9%; Score 1840.4;
ery Match 99.9%; Pred. No. 0;
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16-OCT-2003.
(GETH ) GENENTECH INC.
PLV Match 99.9%; Score 1840.4;
Pred. No. 0;
                                                                                                                                                                                                                                               ADE22238 standard; cDNA; 1857 BP.

CDNA encoding human PRO polypeptide #183.
US2003199056-A1.
23-OCT-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                   ADD79462 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003203428-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding human PRO polypeptide #183.
US2003207417-A1.
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Human PRO polynucleotide #183.
US2003199023-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                   GENENTECH INC.
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Best Local Similarity
RESULT 182
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Best Local Similarity
RESULT 181
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RESULT 180
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RESULT 184
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23-OCT-2003
(GETH ) GEN
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DB 10; Length 1857;
Length 1857;
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Human secreted/transmembrane protein CDNA, #25.
US2003077583-A1.
                                                                                                            PD 16-OCT-2003.

PA (GETH ) GENENTECH INC.

Query Match 99.9%; Score 1840.4;

Best Local Similarity 99.9%; Pred. No. 0;

RESULT 188
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PA (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 99.9%; Pred. No. 0;

RESULT 190
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23-OCT-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
ery Match
99.9%; Pred. No. 0;
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cDNA encoding human PRO polypeptide #183.
US2003199064-A1.
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D ADF97491 standard, cDNA, 1857 BP.

E Human PRO polynucleotide #183.

N US2003207370-A1.

D 06-NOV-2003.

A (GETH ) GENENTECH INC.

Query Match

99.9%; Score 1840.4; DB 10; Length 1857;
     DB 10; Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207384-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADG21515 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207355-A1.
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   99.9%; Score 1840.4; 99.9%; Pred. No. 0;
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Beet Local Similarity 99.9%; Pred. No. 0;
RESULT 204
                                                                                                                                             Score 1840.4;
Pred. No. 0;
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Pred. No. 0;
                                                                                                                                                                                            ADD80566 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003207418-A1.
                                                    ADE42550 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. US2003199032-A1.
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Human PRO polynucleotide #183.
US2001199028-A1.
23-OCT-2003.
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Human PRO polynucleotide #183.
US2003199031-A1.
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Human PRO polynucleotide #183.
US2003194777-A1.
                                                                                     US2003150.
23-OCT-2003.
(GETH ) GENENTECH INC.
1010 99.9%; SC
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(GETH ) GENENTECH INC.
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2003.

LH ) GENENTECH I.

LTY MATCh

Beet Local Similarity >
RESULT 198

ID ADD89594 stand**

Ph Human PRO r

Ph US20031*

Ph 23-C

Ph
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(GETH ) GENENTECH INC.
                                                                                                                                         Query Match
Best Local Similarity 9
RESULT 197
ID ADD80566 standard; CDN
DE CDNA encoding human PH
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
Query Match
Best Local Similarity
RESULT 196
ID ADB42550 standard; cD
DE Human PRO polynucleot
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC
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Best Local Similarity
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Best Local Similarity
RESULT 200
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RESULT 199
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DB 10; Length 1857;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADH55295 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA. US200320731-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human secreted and transmembrane protein PRO301 cDNA. US2032073385-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003207379-A1.
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Human secreted/transmembrane protein cDNA, #25.
US2003064352-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted/transmembrane protein cDNA, #25.
US200303972-A1.
CFEB-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
lery Match 99.9%; Pred. No. 0;
                                                                                                                        99.9%; Score 1840.4; 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                            Score 1840.4;
Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Best Local Similarity 99.9%; Pred. No. 0; RESULT 205
                                                                                                                                                                           CDNA; 1857 BP.
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                               AD680555 standard; cDNA; 1857
Human PRO polynucleotide #183.
US2003207373-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                           Human PRO polynucleotide #183
US2003207372-A1.
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PA (GETH ) GENENTECH INC.

QUERY Match 99.9%;

Best Local Similarity 99.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                    Best Local Similarity
RESULT 206
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Best Local Similarity
RESULT 209
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RESULT 210
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Best Local Similarity
RESULT 211
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Best Local Similarity
                                                                                                                                                                         ADG80003 standard;
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ADM82545 standard; cDNA; 1857 BP.
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RESULT 228
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RESULT 230
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              AD163514 standard, cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207387-A1.
                                                                                                                                 ADH81928 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA. US2003207388-A1.
06-NOV-2003.
                                                                                                                                                                                                                                                        ADH81376 standard; cDNA; 1857 BP.
Wovel human secreted and transmembrane protein PRO301 cDNA. US2003207377-A1.
06-NOV-2003.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003032156-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003040014-A1.
                                                                                        DB 10;
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(GETH ) GENENTECH INC.
2ry Match 99.9%; Score 1840.4;
2ry Match 99.9%; Pred. No. 0;
                                                  OS-NOV-2003.
(GETH) GENENTECH INC.
199.9%; Score 1840.4;
Hery Match 99.9%; Pred. No. 0;
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(GETH ) GENENTECH INC.
17 Match 99.9%; Score 1840.4;
17 Match 99.9%; Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.9%; Score 1840.4; 99.9%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                ACA58993 standard, cDNA, 1857 BP. Human PRO polymucleotide #21. US2002146709-A1.
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13-FBB-2003.
(GETH ) GENENTECH INC.
99.9%;
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20-MAR-2003.
(GETH ) GENENTECH INC.
99.9%;
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(GETH ) GENENTECH INC.
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RESULT 218
                                                                                                 Best Local Similarity RESULT 215
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RESULT 216
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RESULT 219
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Best Local Similarity
RESULT 223
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RESULT 214
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Score 1840.4; DB 12; Length 1857; Pred. No. 0;
                                                                          Length 1857;
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RESULT 225
ID ADNIGE73 standard; CDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 CDNA.
PN US2003087385-A1.
Novel human secreted and transmembrane protein PRO301 cDNA. US2003087355-A1.
                                                                                                                              ADN15944 standard; cDNA; 1857 BP. Novel human secreted and transmembrane protein PRO301 cDNA US2003087353-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US20030873356-Al.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003087357-A1.
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                                                                          DB 11;
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Human secreted/transmembrane protein cDNA, #25.
US2003135025-A1.
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(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
ery Match 99.9%; Pred. No. 0;
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No. 0;
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Pred. No. 0;
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Pred. No. 0;
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(GETH ) GENENTECH INC.
STY MATCh 99.9%; Score 1840.4;
STY MATCh 99.9%; Pred. No. 0;
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ry Match 99.9%; Score 1840.4;
t Local Similarity 99.9%; Pred. No. 0;
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Pred. No. 0;
                                                                                                                                                                                                                          Score
Pred.
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Human PRO polynucleotide #183.
US2003100087-A1.
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08-MAY-2003.

(GETH ) GENENTECH INC.

MATCh ''' 174fty 99.9%;
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15-WAY-2003.
(GETH ) GENENTECH INC.
99.9%;
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Local Similarity 99.9%;
                                    PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.

QUENY MATCh 99.9%;

Best Local Similarity 99.9%;

RESULT 224
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(GETH ) GENENTECH INC.
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US2003199062-A1.
                                                  Query Match
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RESULT 243
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                                         GENENTECH INC.

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Similarity 99.9%; Score 1840.4; DB 12; Length 1857;

Similarity 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted/transmembrane protein cDNA, #25.
US2003129592-A1.
10-JUL-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4; DB 12; Length 1857; st Local Similarity 99.9%; Pred. No. 0;
                                                                                                                                                                                               Length 1857;
                                                                                                                                                                                                                                                                                                                                   DB 12; Length 1857;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE41303 standard; cDNA; 1857 BP.
Human secreted/transmembrane PRO polypeptide cDNA #27.
US2003100497-A1.
                                                                                                                                                                                                 DB 12;
                                                                                                                               #25.
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29-MAY-2003.
(GETH ) GENENTECH INC.
1ery Match 99.9%; Score 1840.4;
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15-MAY-2003.
(GETH) GENENTECH INC.
6ry Match 99.9%; Score 1840.4;
7. ""11arity 99.9%; Pred. No. 0;
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15-MAY-2003.
(GETH ) GENENTECH INC.
18ry Match 99.9%; Score 1840.4;
18ry Match 99.9%; Pred. No. 0;
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(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
rry Match
99.9%; Pred. No. 0;
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10-JUL-2003.
(GETH) GENENTECH INC.
(GETH) GENENTECH INC.
99.9%; Score 1840.4;
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                                                                                                              ADE79620 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA,
US2003130489-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE23342 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003092108-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE23894 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003092110-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE24537 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003092111-A1.
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Best Local Similarity 99.9%; Score
RESULT 235
ID ADE73296 standard; CDNA; 1857 BP.
DE Human secreted/transmembrane protei
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
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Human PRO polynucleotide #183.
US2003203439-A1.
                                                                                                                                                                                                                                            ADE75766 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003211571-A1.
Human PRO polynucleotide #183.
US2003203440-A1.
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Best Local Similarity 9
RESULT 239
ID ADE24537 standar
DE CDNA encodir
PN US2003r
PD 15-
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 238
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Best Local Similarity
RESULT 234
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Best Local Similarity
RESULT 237
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RESULT 241
ID ADE89228 standard;
DE Human PRO polymnole
                                                              Query Match
Best Local Similarity
RESULT 233
                                30-OCT-2003
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23-CCT-2003.
(GETH ) GENENTECH INC.
(ery Match 99.9%; Score 1840.4; DB 12; Length 1857;
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                                 Length 1857;
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                                                                                   ADE41185 standard; cDNA; 1857 BP.
Human secreted/transmembrane polypeptide PRO301 cDNA.
US2003104558-A1.
                                 99.9%; Score 1840.4; DB 12; 99.9%; Pred. No. 0;
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                                                                                                                               US-UNN-2003.
(GETH ) GENENTECH INC.
199.9%; Score 1840.4;
Lery Match 99.9%; Pred. No. 0;
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07-AUG-2003.

(GETH ) GENENTECH INC.

99,9%; Score 1840.4;

ery Match 99.9%; Pred. No. 0;
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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity , 99.9%; Pred. No. 0;
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Human PRO polynucleotide #183.

US2003199061-A1.

23-OCT-2003.

GETH ) GENENTECH INC.

99.9%; Score 1840.4;

st Local Similarity 99.9%; Pred. No. 0;
                                                                                                                                                                                                                             ADE73831 standard, cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA,
US2003148370-A1.
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ID ADE95248 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003199052-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE94696 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003199027-A1.
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Human PRO polynucleotide #183.
US2003199060-A1.
                                                                                                                                                                                                                                                                                                                                                                      ADE18367 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003194794-A1.
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US2003199054-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
23-OCT-2003.
(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 248
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                                            Best Local Similarity RESULT 242
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ID ADE88676 standard;
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23-OCT-2003.
(GETH ) GENENTECH INC.
ery Match 99.9%; Score 1840.4; DB 12; Length 1857;
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(GETH ) GENENTECH INC.
ery Match
99.9%; Score 1840.4; DB 12; Length 1857;
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Query Match 99.9%; Score 1840.4; DB 12; Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003199051-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE91702 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003199058-A1.
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                                                               Score 1840.4; DB 12;
Pred. No. 0;
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Human secreted/transmembrane protein cDNA, #25.
US2003211569-A1.
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Human secreted/transmembrane protein cDNA, #25.
US2003211568-A1.
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Human secreted/transmembrane protein cDNA, #25.
US2003225253-A1.
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Human secreted/transmembrane protein cDNA, #25.
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(GETH ) GENENTECH INC.
17 MATCh 99.9%; Score 1840.4;
27 MATCh 99.9%; Pred. No. 0;
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Pred. No. 0;
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CDNA encoding human PRO polypeptide #183.
23.0CT-2003.
(GETH ) GENENTECH INC.
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13-NOV-2003.
(GETH ) GENENTECH INC.
13-101.
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(GETH ) GENENTECH INC.
99.9%;
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Watch ....itv 99.9%;
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(GODO/) GODOWSKI P J.
(GURN/) GURNEY A L.
(MATH/) MATHER J P.
(WILL/) WILLIAMS P M.
(WODD/) WOOD W I.
L-2003.
Lary Match
Best Local Similarity >
RESULT 251
ID ADF34939 stand>
DE CDNA encod*
PN US2003*
PD 23-
PA
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Best Local Similarity
RESULT 254
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Best Local Similarity
RESULT 253
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Best Local Similarity
RESULT 257
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25-SEP-2003.
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Length 1857;.
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(GETH) GENENTECH INC.
ry Match
#Tocal Similarity 99.9%; Pred. No. 0;
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                                                                                                                                                                           ADG22067 standard; cDNA; 1857 BP. Novel human secreted and transmembrane protein PRO301 cDNA.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003207426-Al.
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Pred. No. 0;
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                    cDNA encoding human PRO polypeptide #183.
US2003207376-A1.
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cDNA encoding human PRO polypeptide #183.
US2003207359-A1.
Best Local Similarity 99.9%; Pred. No. RESULT 259
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Pred.
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Human PRO polynucleotide #183.
US2003207422-A1.
                                  ADG02281 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003207352-A1.
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Human PRO polynucleotide #183.
US2003207353-A1.
                                                                                                                                                                                                                                                                                                                    ADG20137 standard; cDNA; 1857 BP.
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Human PRO polynucleotide #183.
US2003208055-Al.
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06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%; Sr
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) GENENTECH INC.
99.9%; S
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06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%;
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06-NOV-2003.
(GETH ) GENENTECH INC.
MATCh ''Tarity 99.9%;
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(GETH ) GENENTECH INC.
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                                                                                                                                     Best Local Similarity RESULT 260
                                                                                                                                                                                                                                                                                 Best Local Similarity
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Best Local Similarity
RESULT 266
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Best Local Similarity
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99.9%; Score 1840.4; DB 12; Length 1857; 99.9%; Pred. No. 0;
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Novel human secreted and transmembrane protein PRO301 cDNA,
US2003207424-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG23708 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA
US2003207389-A1.
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(GETH ) GENENTECH INC.

iry Match 99.9%; Score 1840.4; DB 12;
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06-NOV-2003.
(GEH) GENENTECH INC.
199.9%; Score 1840.4;
PARC MATCh 99.9%; Pred. No. 0;
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06-NOV-2003.

(GETH ) GENENTECH INC.

99.9%; Score 1840.4;

of nimilarity 99.9%; Pred. No. 0;
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(GETH) GENENTECH INC.
(ETH Match 99.9%; Score 1840.4;
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cDNA encoding human PRO polypeptide #183.
US2003219885-A1.
                                                                                                                                                cDNA encoding human PRO polypeptide #183.
US2003207425-A1.
06-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                         ADG13314 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003207357-A1.
            ADG05210 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003207375-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADF96939 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003207371-A1.
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Human PRO polynucleotide #183.
US2003207374-A1.
                                                                                                                                  ADG19477 standard; cDNA; 1857 BP
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2003.
2003.
2ry Match
Best Local Similarity 5
RESULT 273
ID ADG15541 stand*
DE cDNA encod*
PN US2003**
PD 27-**
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                  Best Local Similarity RESULT 269
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Best Local Similarity
RESULT 271
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Best Local Similarity
RESULT 277
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RESULT 268
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Score 1840.4; DB 12; Length 1857; Pred. No. 0;
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                                                                                                                                  ADG24898 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207427-Al.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207390-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 99.9%; Pred. No. 0; Length RESULT 283
ID ARGG2010 standard; cDNA; 1857 BP.

DE Novel human secreted and transmembrane protein PRO301 cDNA. PN US2003207428-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207356-A1.
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                                                                                                                                                                                                                                                                      ADG07195 standard; cDNA; 1857 BP.
Novel human serreted and transmembrane protein PR0301 US2003207320-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO301
US2003194778-A1.
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                                                                                                                                                                                     06-NOV-2003.
(GETH ) GENENTECH INC.
17 Match 99.9%; Score 1840.4;
17 Match 99.9%; Pred. No. 0;
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(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
99.9%; Pred. No. 0;
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(GETH ) GENENTECH INC.
17 Match 99.9%; Score 1840.4;
17 Match 99.9%; Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
ADG03997 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003207423-A1.
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Human PRO polynucleotide #183.
US2003207358-A1.
                                                                                                                                                                                                                                                                                                                                                                                                             CDNA; 1857 BP
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                                   /82003.
J6-NOV-2003.
(GETH ) GENENTECH INC.
99.9%;
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06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%;
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06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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ID ADG82211 standard; cl
DE Human PRO polynucleol
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC
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Best Local Similarity
RESULT 279
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Best Local Similarity
RESULT 284
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RESULT 286
                                                                                                Best Local Similarity RESULT 278
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Best Local Similarity
RESULT 282
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US2003207805-A1.
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                                                           Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207362-A1.
                                                                                                  ADG56898 standard, cDNA, 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207364-Al.
                                                                                                                                                                                                                                                                                                                                          ABG56554 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207368-A1.
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Novel human secreted and transmembrane protein PRO301 CDNA,
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003207365-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003207420-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003207415-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003207421-A1.
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Pred. No. 0;
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Human secreted/transmembrane protein cDNA, #25.
US2003021146-Al.
06-PEB-2003.
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A. 99.9%; Score 1840.4;

A. 99.9%; Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Human PRO polynucleotide #183.
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06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%; S'
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06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%;
            S20032v.
J6-NOV-2003.
(GETH ) GENENTECH INC.
99.9%;
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06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%;
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 288
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Best Local Similarity
RESULT 290
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Best Local Similarity
RESULT 294
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RESULT 289
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(GETH ) GEN
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ID ADG816
DE Human
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24-52-203.
24-5203.
(GETH ) GENENTECH INC.
ery Match 99.9%; Score 1840.4; DB 12; Length 1857;
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(GETN' ) GENENTECH INC.
17Y Match
1877, Match
187
Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207416-A1.
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US2003207419-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207414-Al.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003207378-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003207429-A1.
                                                                                                                                                                                                                                                                                                                                                                                             Human secreted/transmembrane polypeptide PRO301 cDNA.
US2003180796-A1.
25-SEP-2003.
DB 12;
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Pred. No. 0;
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(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
PY MATCh 99.9%; Pred. No. 0;
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No. 0;
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(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
iry Match 99.9%; Pred. No. 0;
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Pred. No. 0;
99.9%; Score 1840.4; 99.9%; Pred. No. 0;
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Pred. No. 0;
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Pred.
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US2003194793-A1.
                                                                        Human PRO polynucleotide #183.
US2003077723-A1.
                                                                                                                                                                                                                                                                                                                                                                         CDNA; 1857 BP
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25-SER-2003.
(GETH ) GENENTECH INC.
99.9%; F.
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06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%;
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Local Similarity 99.9%;
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   Query Match
Best Local Similarity
RESULT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     ADG63620 standard;
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Best Local S
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Query Match
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                                                                                                                                         DB 12; Length 1857;
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                          DB 12; Length 1857;
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                                                                                                                                                                                                                                                                                               ADG59730 standard; cDNA; 1857 BP.

Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207369-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                               ADG54690 standard; cDNA; 1857 BP.

Novel human secreted and transmembrane protein PRO301 cDNA, US2003230457-A1.
06-NOV-2003.
                                                                                                                                                                                                                                                        DB 12;
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US2004006211-A1.
PA (GETH ) GENENTECH INC.
Query Match 99.9%; Score 1840.4;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 305
                                                              ADH28545 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
30-JAN-2003.
30-JAN-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
                                                                                                                                                                                                                           06-NOV-20Us.
(GETH ) GENENTECH INC.
2ry Match 99.9%; Score 1840.4;
2ry Match 99.9%; Pred. No. 0;
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08-2NA-2004.
08-ZNA-2004.
(GETH) GENENTECH INC.
199.9%; Score 1840.4;
10 99.9%; Pred. No. 0;
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Human secreted/transmembrane protein cDNA,
US2004005553-A1.
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ID ADH59830 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA,
PN US20022155904-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH43486 standard; cDNA; 1857 BP.
Human PRO polynucleotide #27.
US2003224984-A1.
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(GODD/) GODDWARD A.
(GURN/) GURNEY A L.
(MATH/) MATHER J P.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
                                                                         JAN-22331-A1.
JAN-22031.
JAN-2203.
(GETH) GENENTECH IN
BEST LOCAL SIMILARITY 9.
RESULT 306
ID ADG54690 standaring Novel human PN US20037.
PD 06-***
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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GODOWSKI P J.
                                                                                                                                                                                                                                                                Best Local Similarity RESULT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
RESULT 309
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Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207382-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADG09245 standard, cDNA, 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2004009547-A1.
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(GETH ) GENENTECH INC.
(GETH ) ALCh 99.9%; Score 1840.4; DB 12;
(ery Match 99.9%; Pred. No. 0;
                                                                      DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.9%; Score 1840.4; DB 12; 99.9%; Pred. No. 0;
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Human secreted/transmembrane protein cDNA, #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                    #25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted/transmembrane protein cDNA, #25 US2003096340-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #25
                                                                      99.9%; Score 1840.4; 99.9%; Pred. No. 0;
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(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
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22-MAY-2003.
(GETH ) GENENTECH INC.
18FY Match 99.9%; Score 1840.4;
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PA (GETH ) GENENTECH INC.

Query Match 99.9%; Score 1840.4;

Best Local Similarity 99.9%; Pred. No. 0;

RESULT 318
                                                                                                                                                                                                                 Score 1840.4;
Pred. No. 0;
                                                                                                                                                                                                                                                                   ADI18600 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA,
US2003152999-A1.
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Best Local Similarity 99.9%; Pred. No. 0;
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 315
ID ADI65320 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA,
PN US2003148419-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADH97379 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA,
US2003190610-A1.
                                                                                                                                          cDNA encoding human PRO polypeptide #183.
US2003207361-A1.
                                                                                                                           ADI81154 standard; cDNA; 1857 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA; 1857 BP
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06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%;
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15-03N-2004.
(GETH ) GENENTECH INC.
99.9%;
(GURN/) GURNEY A L.
(MATH/) MATHER J P.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-AUG-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 320
                                                                                                                                                                                                                              Best Local Similarity RESULT 314
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RESULT 316
                                                                                     Best Local Similarity
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Length 1857;

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99.9%; Score 1840.4; DB 12; 99.9%; Pred. No. 0;
                                                                                                GETH) GENENTECH INC.

(GETH) GENENTECH INC.

199.9%; Score 1840.4;

197. Match

197. Match

198.9%; Pred. No. 0;
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04-MAR-2004.
(GETH) GENENTECH INC.
199.9%; Score 1840.4;
10rv Match 99.9%; Pred. No. 0;
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PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 334
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03-FEB-2004.
(GETH ) GENENTECH INC.
PRIV MATCh 99.9%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                           ADJ65593 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2004038335-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding human PRO polypeptide #183
US2004048333-A1.
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US2004058424-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADM28315 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2004077064-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO polynucleotide #23. US6686451-B1.
                                                                                                                                                                                            ADK82831 standard; cDNA; 1857 BP.
Human PRO polynucleotide #27.
US2004043927-A1.
                                                    ADJ77471 standard; cDNA; 1857 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA; 1857 BP
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                                                                    Human PRO polynucleotide #183.
US2004038336-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2004.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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GERRITSEN M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOTSTEIN D.
DESNOYERS L.
EATON D L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASHKENAZI A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FERRARA N.
FILVAROFF E.
             Best Local Similarity RESULT 330
                                                                                                                                                        Best Local Similarity RESULT 331
                                                                                                                                                                                                                                                                                                        Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM27729 standard;
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 Query Match
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(GERR/)
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           07-AUG-2003.
(GETH ) GENENTECH INC.
ery Match 99.9%; Score 1840.4; DB 12; Length 1857;
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(GETH ) GENENTECH INC.
ery Match 99.9%; Score 1840.4; DB 12; Length 1857;
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                                                                                                      ADI14700 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207383-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADI18295 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207349-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA. US2004039164-Al.
26-FEB-2004.
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Human secreted/transmembrane protein cDNA, #25.
02-0071-806358-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                ADH60490 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
US2004023331-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AD399547 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
US2003187238-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADM25081 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
US2003096233-A1.
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Human secreted/transmembrane protein cDNA, #25.
US2003190611-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAY-2003.
(GETH ) GENENTECH INC.
17 Match 99.9%; Score 1840.4;
27 Match 99.9%; Pred. No. 0;
                                                                                                                                                 USACCETORS.
06-NOV-2003.
(GETH) GENENTECH INC.
99.9%; Score 1840.4;
ery Match 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.9%; Score 1840.4; 99.9%; Pred. No. 0;
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Pred. No. 0;
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02-OCT-2003.
(GETH ) GENENTECH INC.
99.9%;
                                                                                                                                                                                                                                                                                                                                         (GODD/) GODDARD A.
(GODO/) GODOWSKI P J.
(GURN/) GURNEY A L.
(MATH/) MATHER J P.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-OCT-2003.
(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
RESULT 326
ID ADL08740 standard; cf
DE Human secreted/transm
PN US2003186558-A1.
PD 02-CT-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                      DESNOYERS L.
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Best Local Similarity
RESULT 327
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Best Local Similarity
RESULT 325
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Best Local Similarity
RESULT 323
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                                                               Best Local Similarity RESULT 322
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US2003148371-A1.
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Length 1857;
                                                                                                                         Length 1857;
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                                                                                                                                                                                                                                                   Length 1857;
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                                                                                                                         DB 12;
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   DB 12;
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us-10-785-220b-11.rng.spdi

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(TUMA/) TUMAS D.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
STEWART T A.
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                                                                                           Query Match
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(STEW/)
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RESULT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jin CDNA, #25.

Jin CDNA, #25.

JINA; 1857 BP.

JINA; 1857 BP.

JOURNA; 1857 BP.

JO
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PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 99.9%; Score 1840.4; DB 13; Length 1857;
RESULT 341
ID ADT94259 standard; CDNA, 1857 BP.
DE Human PRO301 cDNA sequence.
PN AU2003259607-A1.
PD 27-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1840.4; DB 13; Length 1857;
Best Local Similarity 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                       99.9%; Score 1840.4; DB 13; Length 1857; 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207354-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          US20050...
24-APR-2003.
(GETH) GENENTECH INC.
GETV MATCh 99.9%; Score 1840.4;
                                                                                                                                                                                                                                                                                                                                                                                        ADI95797 standard; cDNA; 1857 BP.
CDNA encoding human PRO polypeptide #183.
US2003077659-A1.
                                                                                                                                                       (PANJ) PAN J.
(PANJ) PAN J.
(ROYM) ROY M A.
(STEW) STEWART T A.
(TUNA) TUNAS D.
(WILL) WILLIAMS P M.
(WOOD) WOOD W I.
                     GODOWSKI P J.
GRIMALDI C J.
                                                                                                            KLJAVIN I J.
MATHER J P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 339
                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 338
                                                                 GURNEY A L. HILLAN K J.
GODDARD A.
                                                                                                                                                                                                                                                                                                                         Ouery Match
GODD/)
                   GODO/)
                                                                   GURN/)
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99.9%; Score 1840.4; DB 13; Length 1857; 99.9%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1902
                                                                                                                                                                                                                                                                                                                                               DB 4; Length 1902;
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                                                                                                                                                                       DB 4; Length 2259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE08895 standard; DNA; 1902 BP.
Novel DNA-related contig nucleotide sequence #139
WO2003054152-A2.
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.6%; Pred. No. 0;
RESULT 345
ID AAS22710 standard; cDNA; 1902 BP.
DE Human cDNA encoding a novel human protein #276.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                          Human cDNA encoding a novel human protein #275 WO200155437-A2.
                                                                                     Human cDNA encoding a novel human protein #39.
WO200155437-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 99.3%; Score 1829.2;
Best Local Similarity 99.6%; Pred. No. 0;
RESULT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABV28103 standard; cDNA; 3389 BP.
Human prostate expression marker cDNA 28094.
WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV22266 standard; cDNA; 3389 BP.
Human prostate expression marker cDNA 22257.
WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human DNA40628 cDNA encoding PRO301 protein. US2003171568-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.3%; Score 1829.2; 99.6%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.3%; Score 1829.2; 99.6%; Pred. No. 0;
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Local Similarity 99.6%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-2001.
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                        wuery Match
Best Local Similarity , 99.7%; Pred. No. 0;
RESULT 344
                                                                                                                                                                                                                                    AAS22709 standard; cDNA; 1902 BP.
                                                              AAS22473 standard; cDNA; 2259 BP.
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ID ADN35294 standard; DNA; 1842 BP.
DE Human PRO301 gene DNA40628.
PN WO2004031105-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.SEP-2003.
(ASHK/) ASHKENAZI A.
(FONG/) FONG S.
(GODD/) GODDARD A.
(GURN/) GURNEY A L.
(NARI/) NARIER M A.
(TUMA/) TUMAS D.
(WOOD/) WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 347
               Best Local Similarity RESULT 343
                                                                                                                        O 02-AUG-2001.
A (HYSE-) HYSEQ INC.
Query Match
                                                                                                                                                                                                                                                                                                02-AUG-2001.
(HYSE-) HYSEQ INC.
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(HYSE-) HYSEQ INC.
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AAD08335 standard; cDNA; 1918 BP.
Human secreted protein-encoding gene 23 cDNA clone HACAA29, SEQ ID NO:63.
WO200136440-A1.
                 DB 13; Length 3861;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2187;
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Human CD-like molecule HKACI03 cDNA, SEQ ID NO:145.
                                                                                                                                                                    DB 4;
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Human immunoglobulin encoding cDNA SEQ. ID No 30.
WO200155315-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB31509 standard; cDNA; 1812 BP.
Human cDNA encoding a novel protein SEQ ID NO
ÚŞ2003077606-A1.
                                                                                                                                                                                                                         ADK40842 standard, cDNA, 1822 BP.
DNA encoding human platelet F11 receptor #1.
US6699688-B1.
                                                                                                                                                                                                                                                                                                                     97.5%; Score 1796.4; 99.7%; Pred. No. 0;
               99.3%; Score 1812.8; 99.3%; Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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1
1 Similarity 95.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR27640 standard; cDNA; 1822 BP.
Full length human F11 receptor cDNA Seq 6.
WO2004063327-A2.
                                                                                                                      HUMA-) HUMAN GENOME SCI INC.

(HUMA-) HUMAN GENOME SCI INC.

97.7%; Score 1800;

ery Match

99.3%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                 (UYNY ) UNIV NEW YORK STATE RES FOUND
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Human polynucleotide SEQ ID NO 120.
US2002090672-A1.
                                                                                                                                                                                                                                                                                                                                                                            ADN05139 standard; cDNA; 2187 BP.
Antipsoriatic cDNA sequence #785.
WO2004028479-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA06454 standard; cDNA; 1812 BP. Human cDNA SEQ ID NO: 120. WO200154474-A2.
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.2004.
) GENENTECH INC.
97.4%; Sr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KORN/) KORNECKI E.
(BABI/) BABINSKA A.
(EHRL/) EHRLICH Y H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macca
Local Similarity
                             Best Local Similarity RESULT 360
                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 362
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Best Local Similarity
RESULT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (RUBE/) RUBEN C A.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                   02-MAR-2004
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(HUMA-) HUN
                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                            AAD08305 standard; cDNA; 1915 BP.
Human secreted protein-encoding gene 23 cDNA clone HACAA29, SEQ ID NO:33.
WQ200116440-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUK46576 standard; DNA; 3861 BP.
Muman Fl. receptor (Fl1R) transcript variant 4, encoding gene, SEQ ID 7.
02-SEP-2004.
                                                                                                                                                                                                                               ADR46578 standard; DNA; 3794 BP.

Human JAM-1, F11 receptor (F11R) transcript variant 5, encoding gene.
JP200442513-A.
02-SEP-2004.
(DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
(DOKU-) BOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
ery Match
st Local Similarity 99.0%; Score 1824.4; DB 13; Length 3794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR46570 standard; DNA; 3660 BP.
Human JAM-1, F11 receptor (F11R) transcript variant 1, encoding gene.
JP2004242513-A.
(GETH ) GENENTECH INC.

127 Match 99.2%; Score 1827.6; DB 12; Length 1842;

14 Local Similarity 99.5%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.5%; Score 1814.8; DB 13; Length 2141; 99.1%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
ry Match 99.0%; Score 1822.8; DB 13; Length 3660;
t Local Similarity 99.3%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12; Length 2100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2141;
                                                                                                                                                                                    Length 1831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 2141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preparation human clone cDNA, PLACE1005544
                                                                                   ABX93343 standard, cDNA, 1831 BP.
cDNA DNA40628 encoding human A-33 related antigen PRO301.
US2002182206-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12;
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80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GLJUTSU SH
                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 99.1%; Score 1826.2; Best Local Similarity 99.8%; Pred. No. 0; RESULT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GARV-) GARVAN INST MEDICAL RES.

ery Match

98.7%; Score 1817.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1814.8;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.5%; Score 1814.8; 99.1%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK94509 standard; cDNA; 2141 BP.
Human full-length cDNA, SEQ ID NO: 3364.
EP1130094-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL31331 standard; cDNA; 2141 BP.
Full length human cDNA clone SeqID 3364.
EP1396543-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human JAM1 encoding cDNA; 2100 BP.
Human JAM1 encoding cDNA SEQ ID NO:53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beet Local Similarity 99.1%; Prec
RESULT 358
ID ADQ68025 standard; CDNA; 2141 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1130052.
05-SEP-2001.
(HELL-) HELIX RES INST.
98.5%; SC
                                                                                                                                          05-DEC-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 357
         PA (GETH ) GENENTECH 11
Query Match
Best Local Similarity
RESULT 351
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant vector JP2004215665-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-AUG-2004.
(ZOIJ-) ZOIJIN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-SEP-2004
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Best RESULT

BBEE

RESULT

P P P P

DB 6; Length 1421;

DB 3; Length 1421;

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AALSIS98 standard; DNA; 900 BP.
Human junctional adhesion molecule 1 (huJAM1) coding sequence
WO2003008541-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV28136 standard; cDNA to mRNA; 924 BP.
Human junctional adhesion molecule gene.
MO9824897-A1.
11-JUN-1998.
(HOFF) HOFFMANN LA ROCHE & CO AG F.
2TY Match 42.8%; Score 787.6; DB 2; Length 924; St Local Similarity 95.1%; Pred. No. 2.5e-242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2003.
1 (ELIL ) LILLY & CO ELI.
Query Match 48.9%; Score 900; DB 8; Length 900;
Best Local Similarity 100.0%; Pred. No. 1.5e-278;
                                                                                                                                                                                                                                                                                                  AAZ61781 standard; cDNA; 1421 BP.
cDNA encoding human A33 receptor homologue, SEQ ID NO:254.
WO9955865-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL34866 standard; cDNA; 1421 BP.
Human cDNA isolated from skin cells SEQ ID NO: 254
WO200190357-A1.
vuery Match
Best Local Similarity 99.3%; Pred. No. 0;
RESULT 378
ID AAZ61781 standard; CDNA; 1421 BP
DE CDNA encoding human A33 ***
PD 04-NOV-10**
PA NOV-10**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.3%; Score 1350.4; 99.6%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.3%; Score 1350.4; 99.6%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENESIS RES & DEV CORP LTD.
ry Match 73.3%; Score 1350.4;
t Local Similarity 99.6%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.5%; Score 1279.8; 77.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.8%; Score 1047; 1100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.8%; Score 1028; 100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ67404 standard; DNA; 4633 BP.
Human ovarian specific gene SEQ ID NO:118.
02004013311-A2.
(DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D TO TO THE TOTAL T
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T cell activation associated cDNA #35.
WO2004058805-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC99714 standard; cDNA; 1421 BP.
Skin cell cDNA, SEQ ID NO: 254.
WO200069884-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX21837 standard; cDNA; 1140 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-1999.
(SMIK ) SMITHKLINE BEECHAM CORP.
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W09902561-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
RESULT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE07127 standard; DNA; 1943 BP.
Novel coding sequence (useful for identifying genetic disorders) #193.
WO2003054152-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PA (DOKU-) DOKUNITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.

Query Match
Best Local Similarity 99.8%; Pred. No. 0;
D AAX37716 standard; DNA; 2066 BP.
DP Human cDNA clone DNA35936 conserved
DP W09914241-A2.
DP Z5-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADR46572 standard; DNA; 2009 BP.
Human JAM-1, F11 receptor (F11R) transcript variant 4, encoding gene.
JP2004242513-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR46574 standard; DNA; 3527 BP.
Human JAM-1, F11 receptor (F11R) transcript variant 3, encoding gene.
JP2004242513-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 02-SEP-2004.

PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.

Query Match 84.8%; Score 1562.8; DB 13; Length 3527;
Best Local Similarity 92.8%; Pred. No. 0;
RESULT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1943;
                                                                                                                                                                                                                                 91.0%; Score 1675.4; DB 7; Length 1897; 95.8%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.7%; Score 1614.6; DB 2; Length 2066; 99.1%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 1421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 1421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ61675 standard; cDNA; 1421 BP.
cDNA encoding human A33 receptor homologue, SEQ ID NO:70.
WO9955865-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.3%; Score 1663.8; DB 12; 91.8%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL34760 standard; cDNA; 1421 BP.
Human cDNA isolated from skin cells SEQ ID NO: 70.
WO200190357-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.4%; Score 1351.2; 99.3%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GP-NOV-2001.

(HUMA-) HUMAN GENOME SCI INC.

(RTMA-) HUMAN GENOME SCI INC.

(RTM MAtch

(R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.4%; Score 1351.2; 99.3%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                            ADJ67405 standard; DNA; 4249 BP.
Human ovarian specific gene SEQ ID NO:119.
WO2004013311-A2.
12-FEB-2004.
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Human polynucleotide SEQ ID NO 1261.
WO200190304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENESIS RES & DEV CORP LTD.
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Skin cell cDNA, SEQ ID NO: 70.
WO200069884-A2.
                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
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.ATY MATCh
Best Local Similarity S
RESULT 373
ID ABL90699 stand*
DE Human polv*
PN WO201°
PD 29.*
PA
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Best Local Similarity
RESULT 374
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Best Local Similarity
RESULT 371
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Best Local Similarity
RESULT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 377
                                                                                                                                                                                                                                                            Best Local Similarity RESULT 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                          WO200226930-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUL-2003
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DB 12; Length 4633;

DB 12; Length 1236;

DB 2;

DB 6; Length 1421;

DB 4; Length 1421;

Length 726

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ADH62531 standard; DNA; 726 BP.
Human consen01 DNA used to isolate DNA40628 encoding PRO301 protein.
US2003171568-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID AAV28137 standard; cDNA to mRNA; 1374 BP.
DE Mouse junctional adhesion molecule gene.
PN W09824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFWANN LA ROCHE & CO AG F.
Query Match 33.7%; Score 620.6; DB 2; Length 1374;
Best Local Similarity 73.6%; Pred. No. 2e-188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.9%; Score 513.2; DB 8; Length 750; 76.9%; Pred. No. 5.7e-154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vuery Match 34.7%; Score 639; DB 12; Length 726;
Best Local Similarity 98.5%; Pred. No. 1.6e-194;
RESULT 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.7%; Score 639; DB 10; Length 726; 98.5%; Pred. No. 1.6e-194;
PD 03-JUN-1999.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.5%; Pred. No. 1.6e-194;
RESULT 396
                                                                                                                    ABS93346 standard; cDNA; 726 BP.
Consensus sequence expressed sequence tag, EST, consen01
US2002182206-A1.
05-DEC-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.1%; Score 591.2; DB 2; 98.7%; Pred. No. 3.7e-179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lucry match 29.2%; Score 537; DB 12; Best Local Similarity 99.1%; Pred. No. 1.2e-161; RESULT 402
                                                                                                                                                                                                                                  Match 34.7%; Score 639; DB 8;
Local Similarity 98.5%; Pred. No. 1.6e-194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADK40843 standard; cDNA; 721 BP.
DNA encoding human platelet F11 receptor #2.
US6699688-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2004.
(UYNY ) UNIV NEW YORK STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADN35287 standard; DNA; 726 BP.
Human PRO301 DNA fragment consens01.
WO2004031105-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV88991 standard; cDNA; 612 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACA10115 standard; cDNA; 750 BP. Human NOVX polynucleotide #5. WO200290504-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AD008262 standard; cDNA; 750 BP.
Human NOVX polynucleotide #5.
US2004018594-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-1998.
(GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-APR-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                          ASHKENAZI A.
FONG S.
                                                                                                                                                                                                                                                                                                                                                                                                                                     GODDARD A.
GURNEY A L.
NAPIER M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best. Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TUMA/) TUMAS D. (WOOD/) WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST clone IJ638.
WO9845437-A2.
                                                                                                                                                                                                                                     Query Match
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(GURN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB53509 standard, DNA, 1895 BP.
Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4051.
WO2003065993-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-Aug-2003.
(GENE-) GENE LOGIC INC.
17 Match
1895; Pred. No. 2.1e-203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match
35.0%; Score 644.6; DB 13; Length 2453;
Best Local Similarity 73.7%; Pred. No. 5.4e-196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.5%; Score 727.2; DB 4; Length 1894;
Best Local Similarity 71.6%; Pred. No. 1.1e-222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.5%; Score 727.2; DB 6; Length 1894; 71.6%; Pred. No. 1.1e-222;
                                                                                                                                                                                                                                                                                                                                                                                          41.1%; Score 756.6; DB 12; Length 790; 98.4%; Pred. No. 2.2e-232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.5%; Score 708.4; DB 2; Length 1009; 94.7%; Pred. No. 8.6e-217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR46580 standard; DNA; 2453 BP.
Mouse junctional adhesion molecule-1 encoding gene, SEQ ID 11.
JP2004242513-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Length 777;
                                    Length 1116;
                                                                                                                                                                                                              Length 790;
                                                                                                AAK93330 standard; cDNA; 790 BP.
Human cDNA clone representative sequence, SEQ ID NO: 1790
EP1130094-A2.
                                                                                                                                                                                                                                                                                                   5' end of a representative human cDNA cluster SeqID 1790 EP1396543-A2.
                                                                                                                                                                                                  Ouery Match 41.1%; Score 756.6; DB 4; Best Local Similarity 98.4%; Pred. No. 2.2e-232; RESULT 388
                                    42.7%; Score 787; DB 12; 88.5%; Pred. No. 4.3e-242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS22474 standard; cDNA; 777 BP.
Human cDNA encoding a novel human protein #40.
WO200155437-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.7%; Score 657.4; DB 99.8%; Pred. No. 2e-200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX81767 standard; DNA; 726 BP.
Nucleotide sequence used to isolate DNA40628.
WO9927098-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABV83765 standard; cDNA; 1894 BP.
Human polynucleotide SEQ ID NO 94.
US2002090672-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA06428 standard; cDNA; 1894 BP.
Human cDNA SEQ ID NO: 94.
WO200154474-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX21838 standard; cDNA; 1009 BP.
                                                                                                                                                                                                                                                                                                                                              10-MAR-2004.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM CORP.
                (ASAH-) ASAHI KASEI PHARMA CORP
                                                                                                                                                                                                                                                                            ADL29757 standard; cDNA; 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F11 antigen coding sequence. WO9902561-A1.
                                                                                                                                                                       05-SEP-2001.
(HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
RUBE/) RUBEN S M.
A (BARA/) BARASH S C.
Query Match
                                Query Match
Best Local Similarity
RESULT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 393
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-1999
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Length 612;

Length 721;

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ADH62530 standard; DNA; 390 BP.
Human DNA35936 used to isolate DNA40628 encoding PRO301 protein.
US2003171568-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX81766 standard; DNA; 390 BP.
Nucleotide sequence of DNA35936 encoding a A33 related antigen.
WO9927098-A2.
                                                                                                                                                                                                                                                      D Abl6695 standard; DNA; 427 BP.

DE Thyroid cancer related gene sequence SEQ ID NO:5332.

PN W0200194629-A2.

PD 13-DEC-2001.

PA (AVAL.) AVALON PHARM.

Query Match

21.6%; Score 398.6; DB 6; Length 427;

Best Local Similarity 98.6%; Pred. No. 3.4e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABQ57982 standard; cDNA; 612 BP.
Human colon cancer related nucleotide sequence SEQ ID NO:1677.
WO200229086-A2.
                                            Length 427;
                                                                                                                                                                                                                Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 459;
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Best Local Similarity 100.0%; Pred. No. 1.9e-114;
RESULT 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 390;
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Best Local Similarity 100.0%; Pred. No. 1.9e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABX993345 standard; cDNA; 390 BP.
Consensus assembly expressed sequence tag, EST, DNA35936.
US2002182206-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID AAX37715 standard; DNA; 390 BP.
DE Human cDNA clone DNA35936.
BN WOS914241-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Query Match
21.2%; Score 390; DB 2; L4
BBST Local Similarity 100.0%; Pred. No. 1.9e-114;
                                     Ouery Match 21.6%; Score 398.6; DB 2; Best Local Similarity 98.6%; Pred. No. 3.4e-117; RESULT 410
                                                                                                                                                                                                 Query Match
21.6%; Score 398.6; DB 6;
Best Local Similarity 98.6%; Pred. No. 3.4e-117;
RESULT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A (GETH ) GENENTECH INC.
Query Match 21.6%; Score 397.6; DB 2;
Best Local Similarity 97.3%; Pred. No. 7.6e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 21.3%; Score 391.8; DB 6; Best Local Similarity 96.3%; Pred. No. 6.7e-115;
                                                                                                   ABL66127 standard; DNA; 427 BP.
Lung cancer related gene sequence SEQ ID NO:4464
WO200194629-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX56583 standard; DNA; 459 BP.
Human AA149993.RC DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUN-1999.
(GETH ) GENENTECH INC.
25-MAR-1999.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-DEC-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                 13-DEC-2001.
(AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-SEP-2003.
(ASHK/) ASHKENAZI A.
(FONG/) FONG S.
(GODD/) GODDARD A.
(GURN/) GURNEY A L.
(NAPI/) NAPIER M A.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GURNEY A L.
NAPIER M A.
TUMAS D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-APR-2002.
(FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A (TUMA/) TUMAS D.
A (WOOD/) WOOD W I.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-1999
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PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 26.8%; Score 492.8; DB 12; Length 605;
Best Local Similarity 97.6%; Pred. No. 1.9e-147;
RESULT 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 27.9%; Score 513.2; DB 12; Length 750; Best Local Similarity 76.9%; Pred. No. 5.7e-154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vuery Match 26.8%; Score 492.8; DB 4; Length 605; Beet Local Similarity 97.6%; Pred. No. 1.9e-147; RESULT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.7%; Score 399.2; DB 2; Length 428; 98.8%; Pred. No. 2.2e-117;
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ID AAX56563 standard; DNA; 428 BP.
DE Human N20044.RC DNA fragment PN W09914241.A2.
PD 25-MAR-1900
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PA (GETH) GENENTECH INC.

Query Match

22.4%; Score 412.4; DB 2;

Best Local Similarity 93.2%; Pred. No. 1.4e-121;

RESULT 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA 5'-end sequence, SEQ ID NO: 660.
EP1130094-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5' end of a human cDNA molecule SeqID 660.
EP1396543-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX56579 standard; DNA; 529 BP.
Human T86963.RC DNA fragment.
WO9914241-A2.
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Human AA244018.RC DNA fragment.
WO9914241-A2.
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Human AA101562.RC DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK92200 standard; cDNA; 605
                                                                                                                                                                                                                                                            (LLUX/) LLU A.V. MALYANKAR U M. MILLER C E. MILL/) MILLER T I. (PADI/) MILLER T I. (PADI/) PADIGARU M. (PENA/) PENA C E A. (FREG/) SHENGY S G. (SHIM/) SHENGY S G. (SHIM/) SHENGY S G. (TAUP/) PADIER K A. (TAUP/) TAUPIER K A. (TAUP/) VERNET C A M. (VOSS/) VOSS E Z. (ZERH/) ZERHUSEN B D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST.
               BURGESS C E. CASMAN S J. CHAPOVAL A. EDINGER S R. GERLACH V. GORMAN L. GUNTHER E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 409
                                                                                                                                                                                          KEKUDA R.
LEPLEY D M.
                                                                                                                                                                      GUO X S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-SEP-2001
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                                                                                                                            GORM/)
                                                                                                                                                                    COOX/)
                                                                                                                                                                                          KEKU/)
                                                                                                                                                                                                                                                      rinx/
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20.7%; Score 382; DB 4; Length 382; 100.0%; Pred. No. 7.2e-112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.7%; Score 382; DB 5; Length 382; 100.0%; Pred. No. 7.2e-112;
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     Best Local Similarity 100.0%; Pred. No. 7.2e-112; RESULT 427
                                                                                                                                                                                             Prostate cancer therapy associated cDNA #135.
US2002192763-A1.
19-DBC-2002.
                                          AAH84805 standard; cDNA; 382 BP.
Human prostate-specific cDNA sequence P185.
WO200134802-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL94955 standard; cDNA; 382 BP.
Human P185 cDNA sequence SEQ ID NO 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 431
ID ABS58664 standard, cDNA; 382 BP.
DE Prostate tumour cDNA #135.
                                                                                                                                                                               ACA59392 standard; cDNA; 382 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS10134 standard; cDNA; 382 BP.
Human prostate tumour cDNA #25.
US6262245-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
FOY T M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HENDERSON R A. HURAL J.
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DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
WANG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DILLON D C.
MITCHAM J L.
HARLOCKER S I
                                                                                            17-MAY-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                        STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                  MITCHAM J L.
HARLOCKER S
                                                                                                                                                                                                                                                                                                                  JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                        Best Local Similarity RESULT 428
                                                                                                                                                                                                                                                    XU J.
DILLON D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
RESULT 430
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RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JIANG Y.
KALOS M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                       CARTER D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human P185 CDNA
US2002022248-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-FEB-2002
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                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DBAS/)
(FOYT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SKEI/)
.(HEPL/)
                                                                                                                                                                                                                                                                                                                      JIAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HEND/)
                                                                                                                                                                                                                                                                                                    HARL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JIAN/
KALO/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LISX/
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LISX/
WANG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCNE/
                                                                                                                                                                                                                                                  (XOO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKEI/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HURA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FANG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA06375 standard; cDNA; 382 BP.
Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:139.
WO200004149-A2.
                                                                                                                                                                                                                                                                 Length 387;
                                                                                   | 15-APR-2004.
| GETH | GENENTECH INC.
| ery Match | 21.2%; Score 390; DB 12; Length 390; | ery Match | 21.2%; Pred. No. 1.9e-114;
                                                                                                                                                                                                                                                                                                                                                                                                    20.7%; Score 382; DB 2; Length 382; 100.0%; Pred. No. 7.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.7%; Score 382; DB 4; Length 382; 100.0%; Pred. No. 7.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.7%; Score 382; DB 2; Length 382; 100.0%; Pred. No. 7.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.7%; Score 382; DB 3; Length 382; 100.0%; Pred. No. 7.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.7%; Score 382; DB 4; Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH02556 standard; cDNA; 382 BP.
Prostate tumour antigen determined cDNA sequence for P185.
W0200125272-A2.
12-APR-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate tumour protein partial DNA sequence #131.
US2002090372-A1.
                                                                                                                                                                                                                   MUSALLE...
25-MAR-1999.
(GETH ) GENENTECH INC.
(GETY MATCh 20.9%; Score 384.4; DB 2;
(ery Match 29.7%; Pred. No. 1.2e-112;
       100.0%; Pred. No. 1.9e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.7%; Score 382; DB 3; L 100.0%; Pred. No. 7.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.7%; Score 382; DB 4; I 100.0%; Pred. No. 7.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Avanys491 standard; cDNA; 382 BP.
Human prostate-specific cDNA sequence P185.
WO200151633-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV61227 standard; cDNA; 382 BP, cDNA sequence of prostate tumour clone. WO9837093-A2.
                                                                                                                                                                                                                                                                                                               AAV58612 standard; cDNA; 382 BP.
Prostate tumour specific gene clone.
WO9837418-A2.
                                     ADN35286 standard; DNA; 390 BP.
Human PRO301 DNA fragment DNA35936.
WO2004031105-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate cDNA sequence #135.04-00m-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABS71280 standard; cDNA; 382 BP.
                                                                                                                                                                            AAX56535 standard; DNA; 387 BP.
Human AA152150 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                             PD 27-AUG-1998.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2-A2.
2001.
201.
21-) CORIXA CORP.
2-ry Match
Best Local Similarity 126
ID AAH02556 standa-
DE Prostate time PN WO20012-
PD 12-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-1998.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-2000.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2001.
(CORI-) CORIXA CORP.
Best Local Similarity
RESULT 418
                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
RESULT 424
                                                                                                                                        Best Local Similarity RESULT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DILL/) DILLON D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                            Query Match
                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ61659 standard; cDNA; 403 BP. cDNA encoding human skin cell transmembrane protein, SEQ ID NO:54 WO9955865-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Neco. .

WOOM1421-192.

25-MAR-1999.

(GETH ) GENENTECH INC.

20.3%; Score 373.2; DB 2; Length 467;

lery Match ....1arity 97.0%; Pred. No. 5.6e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-NOV-2001.
(GENE-) GENESIS RES & DEV CORP LTD.
ery Match 20.7%; Score 380.4; DB 6; Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 20.7%; Score 380.4; DB 4; Length 403; Best Local Similarity 99.7%; Pred. No. 2.4e-111; RESULT 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.7%; Score 380.4; DB 3; Length 403, 99.7%; Pred. No. 2.4e-111;
                                                                                                                                                                                                                                                                                                                            20.7%; Score 382; DB 10; Length 382; 100.0%; Pred. No. 7.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.5%; Score 378; DB 2; Length 415; 99.0%; Pred. No. 1.5e-110;
                                                                                                                                                                                              20.7%; Score 382; DB 8; Length 382; 100.0%; Pred. No. 7.2e-112;
                                                                Length 382;
                                                                                                              ACC95119 standard, cDNA, 382 BP.
Prostate tumour specific cDNA sequence SEQ ID 139.
WO200289747-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL34744 standard; cDNA; 403 BP.
Human cDNA isolated from skin cells SEQ ID NO: 54
WQ200190357-Al.
                                                              20.7%; Score 382; DB 6; Lv 100.0%; Pred. No. 7.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.7%; Score 382; DB 10; 100.0%; Pred. No. 7.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-NOV-2000.
(GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                        ADG26005 standard; CDNA, 382 BP.
Human prostate-specific CDNA #135.
21-AUG-2003.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                              ADB13589 standard; cDNA; 382 BP.
Human prostate specific cDNA P185.
US2003185830-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC99592 standard; cDNA; 403 BP.
Skin cell cDNA, SEQ ID NO: 54.
WO200069884-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX56542 standard; DNA; 467 BP.
Human N28398 DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX56502 standard; DNA; 395 BP.
Human W76302 DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX56510 standard; DNA; 415 BP.
Human AA101561 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2S-MAR-1999.
(GETH ) GENENTECH INC.
      xu J, xu J.

LuL/, DILLON D C.

Lory Match
Best Local Similarity RESULT 432
ID ACC95119 stander
D P Prostate tor
PN W020028*
PN W020028*
PN WP20028*
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 44
ID AD026005 standard; CDP
DE Human prostate-specifi
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2002081580-A1.
27-JUN-2002.
(XUJJ/) XU J.
(DILL/) DILLON D C.
                                                                                                                                                            14-NOV-2002.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                             02-OCT-2003.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 436
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                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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AAH87415 standard; DNA; 327 BP.
Human single nucleotide polymorphism containing DNA sequence #2272.
WO9953095-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH85597 standard; DNA; 327 BP.
Human single nucleotide polymorphism containing DNA sequence #454.
W09953095-A2.
                                                                             ID AAX56574 standard; DNA; 341 BP.
DE Human 140695.RC DNA fragment.
PN W09914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 99.4%; Pred. No. 1.2e-97;
RESULT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AALO0711 standard; cDNA; 425 BP.

Human reproductive system related antigen cDNA SEQ ID NO: 712.
W0200155320-A2.

(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T.OCT.1999.

(WHED ) WHITEHEAD INST BIOMEDICAL RES.

ery Match

17.6%; Score 323.8; DB 2; Length 327;

ery Match

17.6%; Pred. No. 3.7e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD 21-OCT-1999.

PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

Query MAtch 17.6%; Score 323.8; DB 2; Length 327;

Best Local Similarity 99.4%; Pred. No. 3.7e-93;

RESULT 447
                                                                                                                                                                                                                                                                                                                                                                                      Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.4%; Score 320.8; DB 4; Length 425; 98.5%; Pred. No. 4e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 425;
                                        Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 18.0%; Score 330.8; DB 2; Best Local Similarity 98.9%; Pred. No. 2.2e-95; RESULT 444
D ACHJO092 standard; cDNA; 416 BP.
                                                                                                                                                                                                                                                                                                                                                                      Uuery Match
18.2%; Score 335.6; DB 2;
Best Local Similarity ' 96.4%; Pred. No. 7.6e-97;
RESULT 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.4%; Score 320.8; DB 4; 98.5%; Pred. No. 4e-92;
                                        19.2%; Score 354; DB 2; I 99.5%; Pred. No. 7.7e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.9%; Score 330; DB 9; 95.6%; Pred. No. 4.3e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS28818 standard; cDNA; 425 BP.
Human immunoglobulin encoding cDNA SEQ ID No
WO200155315-A2.
                                                                                                                                                                                                                                                                             AAX56577 standard; DNA; 503 BP.
Human R72982 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX56559 standard; DNA; 358 BP.
Human AA483522.RC DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DE Human teetis cDNA #478.

PN US2003073623-A1.

PA (DRWA/) DRWANAC R T.

PA (LABA/) LABAT I.

PA (STRC/) STACHS-CRAIN B.

PA (UNCK/) DICKSON M C.

PA (GONE/) JONES L W. 17.9

QUETY MATCH
25-MAR-1999.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-1999.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                     Best Local Similarity RESULT 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
RESULT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              25-MAR-1999
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                                        Query Match
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Best Local Similarity 87.4%; Pred. No. 3e-85; RESULT 458
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24-APR-2003.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
17.4%; Score 320.8; DB 10; Length 425;
criffing 98.5%; Pred. No. 4e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAR-2003.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
17.4%; Score 320.8; DB 11; Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-WAR-1999.
(GETH ) GENENTECH INC.
16.3%; Score 299.6; DB 2; Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD 25-MAR-1999.

PA (GETH ) GENENTECH INC.

QUETY MATCh 17.4%; Score 320.4; DB 2; Length 322;

B88t Local Similarity 99.7%; Pred. No. 4.6e-92;

RESULT 455
                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
ry Match
17.4%; Score 320.8; DB 5; Length 425;
t Local Similarity 98.5%; Pred. No. 4e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.4%; Score 320.8; DB 6; Length 425; 98.5%; Pred. No. 4e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 16.8%; Score 310.2; DB 2; Length 435; Best Local Similarity 97.2%; Pred. No. 1.1e-88; RESULT 457
                                                                                                                                        Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-2001.

1 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match
17.3%; Score 318; DB 5; Length 394;

Best Local Similarity 100.0%; Pred. No. 3.1e-91;
                                                                                                                                                                                                 AAS40130 standard; cDNA; 425 BP.
DNA encoding human prostate cancer antigen, Seq ID No 71
W0200155316-A2.
02-ANG-2001.
                                                                                  02-AUG-2001.
(HUWA-) HUMAN GENOME SCI INC.
(HUWA-) HUMAN 17.4%; Score 320.8; DB 4;
ery Match 17.4%; Score 320.8; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB31543 standard; CDNA; 425 BP.
Human cDNA encoding a novel protein SEQ ID NO 64.
US2003077606-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate cancer associated gene SegID71. US2003054373-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV42676 standard, cDNA; 394 BP.
Human prostate expression marker cDNA 42667.
WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                ABV83787 standard; cDNA; 425 BP.
Human polynucleotide SEQ ID NO 116.
US200209672-A1.
11-JUL-2002.
                       ABA06450 standard; cDNA; 425 BP.
Human cDNA SEQ ID NO: 116.
WO200154474-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA; 322 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX56552 standard; DNA; 504 BP.
Human AA224590.RC DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA; 435 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ09125 standard; DNA; 425 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX56529 standard; DNA; 32
Human 979636 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX56524 standard; DNA; 43
Human T87045 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-1999.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 454
                                                                                                                                                   Best Local Similarity RESULT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RUBE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 452
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
      RESULT 449
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Query Match 15.5%; Score 286.4; DB 6; Length 1009; Best Local Similarity 73.2%; Pred. No. 8.3e-81;
                                         PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 299.2; DB 2; Length 408;
Best Local Similarity 91.0%; Pred. No. 3.6e-85;
RESULT 459
                                                                                                                                                                                                                            GETH ) GENENTECH INC. (GETH ) GENENTECH INC. ery Match 15.8%; Score 291.4; DB 2; Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PD 25-MAR-1999.

PA (GETH ) GENENTECH INC.

Query Match 15.4%; Score 284.4; DB 2; Length 286;

Best Local Similarity 99.7%; Pred. No. 1.7e-80;

RESULT 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 15.5%; Score 285.8; DB 2; Length 289; Local Similarity 99.3%; Pred. No. 6.1e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.2%; Score 280.4; DB 2; Length 282; 99.6%; Pred. No. 3.3e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 293;
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                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
Query Match
15.8%; Score 291; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 1.3e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e-79;
RESULT 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 291; DB 2;
Pred. No. 1.3e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN74213 standard; cDNA; 1009 BP.
Bovine embryonic germ (EG) cell cDNA EST #264.
WG200194550-A2.
(INPI-) INPIGEN INC.
                                                                                                                                                                                                                                                                                                                                        AAX56539 standard; DNA; 291 BP. Human 1818676 DNA fragment. WO-9914241.A2. 25-MRR-1999.
AAX56587 standard; DNA; 408 BP.
Human R01692.RC DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 461
ID AAX37719 standard; DNA; 293 BP.
DE Human clone T87045 DNA.
PN W09914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX56566 standard; DNA; 286 BP.
Human 3212856 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX56532 standard; DNA; 281 BP.
                                                                                                                                                                     DNA; 296 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 282 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-1999.
(GETH ) GENENTECH INC.
ery Match
st Local Similarity 99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 463
ID AAXS6572 standard; DNA; 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human 2925803 DNA fragment WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX56576 standard; DNA; 282
Human 3144865 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human 1793273 DNA fragment WO9914241-A2.
                                                                                                                                                                     AAX56554 standard; DNA; 29
Human 930239 DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-1999.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
                                                                                                                                                                                                               WO9914241-A2.
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PD 25-MAR-1999.

PA (GETH ) GENENTECH INC.

QUETY MATCh 15.2%; Score 279.8; DB 2; Length 378;

Best Local Similarity 91.1%; Pred. No. 6.1e-79;

RESULT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 14.8%; Score 273.4; DB 2; Length 287;
Best Local Similarity 99.3%; Pred. No. 6e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD 25-MAR-1999.

PA (GETH ) GENENTECH INC.

Query Match 14.5%; Score 267.4; DB 2; Length 269;

Best Local Similarity 99.6%; Pred. No. 4.9e-75;

RESULT 473
                                                                                                                                                                                                                                                                                                                                                                                                          vuery Match
14.9%; Score 273.6; DB 2; Length 528;
Best Local Similarity 79.7%; Pred. No. 7.5e-77;
RESULT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 14.2%; Score 260.8; DB 2; Length 264; Best Local Similarity 99.2%; Pred. No. 6.5e-73; RESULT 475
                                                                                                                                                                                                                                      Query Match 14.9%; Score 275; DB 2; Length 275; Best Local Similarity 100.0%; Pred. No. 1.8e-77; RESULT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 14.1%; Score 260; DB 2; Length 260; Best Local Similarity 100.0%; Pred. No. 1.2e-72; RESULT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 269;
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PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 99.6%; Pred. No. 3.2e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX56531 standard; DNA; 269 BP.
Human 2328920 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX56517 standard; DNA; 260 BP.
Human 3236257 DNA fragment.
W09914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX56522 standard; DNA; 261 BP.
Human 1731885 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX56562 standard; DNA; 264 BP.
Human 1283885 DNA fragment.
WO9914241-A2.
              AAX56590 standard; DNA; 378 BP.
Human T84017.RC DNA fragment.
WO9914241-A2.
                                                                                                                                                                      AAX56538 standard; DNA; 275 BP.
Human 956595 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX56565 standard; DNA; 287 BP.
Human 2025350 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX56557 standard; DNA; 269 BP.
Human 1004380 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                             DNA; 528 BP.
                                                                                                                                                                                                                                                                                                                           AAX56570 standard; DNA; 528
Human AA244075 DNA fragment.
WO9914241-A2.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 467
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PD 25-MAR-1999.

PA (GETH ) GENENTECH INC.

QUERY MATCh

Best Local Similarity 99.6%; Pred. No. 1.6e-70;

RESULT 482

ID AAX6514 standard; DNA; 252 BP.

PN W09914241-A2.

PD 25-MAR-1999.

PA (GETH ) GENENTECH INC.

QUERY MATCh

Best Local Similarity 100.0%; Pred. No. 4.4e-70;

RESULT 483
ID AAX56589 standard; DNA; 274 BP.

DE Human AA.101520.RC DNA fragment.

PN W09914241-42.

PD 25-WAR-1999.

PA (GETH ) GENENTECH INC.

Query Match

14.0%; Score 258.4; DB 2; Length 274;

RESULT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD 14-MXY-1998.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match
Best Local Similarity 99.6%; Pred. No. 1.2e-69;
ID AAX114AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PD 25-WAR-1999.

PA (GETH ) GENENTECH INC.

Query Match 13.8%; Score 254.4; DB 2; Length 256;

Best Local Similarity 99.6%; Pred. No. 7.4e-71;

RESULT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 13.8%; Score 254.4; DB 2; Length 256; Best Local Similarity 99.6%; Pred. No. 7.4e-71; RESULT 481
                                                                                                                                                                                                                                                   PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 258; DB 2; Length 271;
Best Local Similarity 99.6%; Pred. No. 5.3e-72;
RESULT 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PN WOS914241-22.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 4.4e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 14.0%; Score 257; DB 2; Length 257; Best Local Similarity 100.0%; Pred. No. 1.1e-71; RESULT 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAXI1439 standard; DNA; 251 BP.
Human biallelic polymorphic DNA fragment WI-8024c.
WO9820165-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX56558 standard; DNA; 256 BP. Human 1217411 DNA fragment. w09914241-A2. 25-MAR-1999. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX56569 standard; DNA; 255 BP.
Human 1804959 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                 AAX56503 standard; DNA; 271 BP.
Human 3124762 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                             AAX56551 standard; DNA; 257 BP.
Human 1424836 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX56573 standard; DNA; 256 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX56507 standard; DNA; 257 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human 1345563 DNA fragment WO9914241-A2.
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(GETH ) GENENTECH INC.
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25-MAR-1999.
(GETH ) GENENTECH INC.
     WO9914241-A2.
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                                                                                                                                                                                                                               2; Length 252;
                                                                                                                                                                                                                                                                                                                                                                                  Length 312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.4%; Score 247.4; DB 2; Length 257; 96.5%; Pred. No. 1.3e-68;
                                                                              Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 250; DB 2; Length 360; Pred. No. 2.4e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 250;
                                                                                                                                                                                                                                                                            DE Human 014756 DNA fragment.

PN WOS914241-A2.

PN WOS914241-A2.

PD 25-WAR-1999.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 96.0%; Pred. No. 1.9e-69;

RESULT 488

ID AAX56521 standard, DNA, 250 BP.

DE Human 2345419 DNA fragment.
                   PD 14-MAY-1998.

PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.

Query Match 13.6%; Score 250.6; DB 2;

Best Local Similarity 99.6%; Pred. No. 1.2e-69;

RESULT 486
Human biallelic polymorphic DNA fragment WI-8024b WO9820165-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD 25-MAR-1999.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 98.4%; Pred. No. 2.6e-69;

RESULT 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH) CENENTECH INC.

ry Match

t Local Similarity 100.0%; Pred. No. 1.9e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.6%; Score 250; DB 2; Best Local Similarity 100.0%; Pred. No. 1.9e-69; RESULT 489
                                                                                                                                                                    PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 99.6%; Pred. No. 1.4e-69;
                                                                                                                               AAX56555 standard; DNA; 252 BP.
Human 876764 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX56547 standard; DNA; 360 BP.
Human R28222 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX56513 standard; DNA; 257 BP.
Human 492141 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX37718 standard; DNA; 250 BP.
Human clone 2345419 DNA.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA; 256 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX56519 standard; DNA; 247 BP.
Human 1452523 DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX56525 standard, DNA, 252
Human 1932979 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX56509 standard; DNA; 256
Human 2197534 DNA fragment.
WO9914241-A2.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 494
ID AAXS6510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-1999
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PD 25-MAR-11999.

PA (GETH ) GENENTECH INC.

13.4%; Score 246.6; DB 2; Length 255;

Best Local Similarity 98.0%; Pred. No. 2.4e-68;

RESULT 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 239.4; DB 2; Length 241; Pred. No. 4.9e-66;
                                                                                                                                                                                                                                                                                                         PD 25-WAR-1999.

PA (GETH ) GENENTECH INC.

QUELY MAtch 13.3%; Score 245.4; DB 2; Length 248;

Best Local Similarity 99.2%; Pred. No. 5.8e-68;

RESULT 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.2%; Score 242.4; DB 2; Length 256; Best Local Similarity 99.2%; Pred. No. 5.4e-67; RESULT 499
Query Match 13.4%; Score 247; DB 2; Length 247; Best Local Similarity 100.0%; Pred. No. 1.8e-68; RESULT 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 12.9%; Score 237; DB 2; Length 237; Local Similarity 100.0%; Pred. No. 2.9e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZS-MAR-1999.
(GETH ) GENENTECH INC.
13.0%; Score 240; DB 2; L.
100.0%; Pred. No. 3.le-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MR-1999.
(GETH ) GENENTECH INC.
(GETY Match 13.2%; Score 244; DB 2;
ery Match 99.6%; Pred. No. 1.6e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 240; DB 2;
Pred. No. 3.3e-66;
                                                                                                                                                                                                                                              AAXS6585 standard; DNA; 248 BP.
Human 2223391 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX56560 standard; DNA; 256 BP.
Human 732999 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAXS6568 standard, DNA; 241 BP.
Human 1807742 DNA fragment.
WO9914241-A2.
                                                                           AAXS6581 standard; DNA; 255 BP.
Human 647074 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX56506 standard, DNA; 259 BP.
Human 3234064 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                  DNA; 245 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX56544 standard; DNA; 240 BP.
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Human 1282058 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PA (GETH ) GENENTECH INC.
Query Match 13.0%;
Best Local Similarity 99.6%;
RESULT 501
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ry Match
13.0%;
rt Local Similarity 99.6%;
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Human 1274809 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                            AAXS6540 standard; DNA; 245
Human 2220993 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human 3240004 DNA fragment.
WO9914241-A2.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-1999
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(GÉTH ) GEN
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(GETH ) GENENTECH INC.
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PD 25-MAR-1999.

PA (GETH) GENENTECH INC.

Query Match
12.9%; Score 236.8; DB 2; Length 240;
Best Local Similarity 99.2%; Pred. No. 3.3e-65;
RESULT 504
ID AAX56505 standard; DNA; 268 BP.
DE Human 777818 DNA fragment.
PN W09914241-A2.
PD 25-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Query Match
12.5%; Score 230.4; DB 2; Length 232;
Best Local Similarity 99.6%; Pred. No. 3.8e-63;
                                                                                                                                                                                                                                                                                                                   Query Match 12.6%; Score 232.6; DB 2; Length 268; Best Local Similarity 92.6%; Pred. No. 8.1e-64; RESULT 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.2%; Score 224.4; DB 2; Length 226;
Best Local Similarity 99.6%; Pred. No. 3.2e-61;
RESULT 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-62;
RESULT 508

DE Human 2797137 DNA fragment.
PD 55-MAR-1999.
PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 224; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 4.3e-61;
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PA (GETH ) GENENTECH INC.
Query Match Match 12.1%; Score 223; DB 2; Length 430;
Best Local Similarity 82.5%; Pred. No. 1.3e-60;
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PA (GETH ) GENENTECH INC.

Query Match

12.1%; Score 223; DB 2; I
Best Local Similarity 100.0%; Pred. No. 8.9e-61;

RESULT 511
                                                                                                                                                                                                                                                                                                                                                                                           AXX56550 standard; DNA; 264 BP.

Human T39606 DNA fragment.
W09914241-A2.
25-MAR-1999.
ECTH ) GENENTECH INC.
ETH ) GENENTECH SE, Score 230.8; DB
st Local Similarity 95.2%; Pred. No. 3e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX56586 standard; DNA; 232 BP.
Human 1447744 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX56541 standard; DNA; 224 BP.
Human 1706515 DNA fragment.
WO9914241-A2.
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Human clone 1508565 DNA.
25-MAR-1999.
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Human AA227408 DNA fragment.
WO9914241-A2.
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Human 767739 DNA fragment.
WO9914241-A2.
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Human R02633 DNA fragment.
W09914241-A2.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 506
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/ Match 11.7%; Score 215.6; DB 12; Length 581; Local Similarity 82.9%; Pred. No. 3.9e-58;
                                                                                                                                                                                                                                                                                                                  PD 25-MAR-1999.
AA (GETH ) GENENTECH INC.
Query Match 11.9%; Score 219.4; DB 2; Length 271;
Best Local Similarity 94.6%; Pred. No. 1.5e-59;
RESULT 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 11.7%; Score 215.6; DB 4; Length 581; Best Local Similarity 82.9%; Pred. No. 3.9e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Query Match 11.8%; Score 217; DB 2; Length 235;
Best Local Similarity 96.6%; Pred. No. 7.9e-59;
RESULT 516
                                                                                                                                               PD 25-MAR-1999.

PA (GETH ) GENENTECH INC.

11.9%; Score 220; DB 2; Length 220; Best Local Similarity 100.0%; Pred. No. 8.2e-60;

RESULT 514

ID AAX56575 standard; DNA; 271 BP.

DE Human R27969.RC DNA fragment.

PN 909314241-A2.
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(GETH) GENENTECH INC.
11.6%; SCORE 213; DB 2; Length 236;
st Local Similarity 98.2%; Pred. No. 1.5e-57;
Query Match 11.9%; Score 220; DB 2; Length 220; Best Local Similarity 100.0%; Pred. No. 8.2e-60; RESULT 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 216.2; DB 2;
Pred. No. 1.4e-58;
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Best Local Similarity 96.0%; Pred. No. 3.7e-58;
RESULT 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK92951 standard; cDNA; 581 BP.
Human cDNA 3'-end sequence, SEQ ID NO: 1411.
EP1130094-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADL29378 standard; cDNA; 581 BP.
3' end of a human cDNA molecule SegID 1411.
EP1396543-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX56556 standard; DNA; 239 BP.
Human 159097 DNA fragment.
WO9914241-A2.
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Human 2044611.RC DNA fragment.
WO9914241-A2.
                                                                        AAX56526 standard; DNA; 220 BP.
Human 1508565 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX56553 standard; DNA; 235 BP.
Human 929944 DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA; 262 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-1999.
(GETH ) GENENTECH INC.
Ery Match
St Local Similarity 96.6%;
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Human AA215609 DNA fragment
WO9914241-A2.
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(HELI-) HELIX RES INST.
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(GETH ) GENENTECH INC.
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(HUMA-) HUMAN GENOME SCI INC.

(HUMA-) HUMAN GENOME SCI INC.

10.6%; Score 195.6; DB 4; Length 367;
                                                                                                                                                                                                                                                                                                         vuery Match 11.2%; Score 206.8; DB 2; Length 234;
Best Local Similarity 98.3%; Pred. No. 1.5e-55;
RESULT 524
Query Match 11.4%; Score 209.2; DB 2; Length 243; Best Local Similarity 96.7%; Pred. No. 2.6e-56; RESULT 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vuery Match
Best Local Similarity 87.8%; Pred. No. 4.8e-54;
RESULT 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.9%; Score 201.4; DB 2; Length 203; 99.5%; Pred. No. 7.7e-54;
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                                                                                                                                                               Length 219;
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
ery Match 10.9%; Score 200.2; DB 5;
ery match 98.1%; Pred. No. 2.2e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
ry Match 10.9%; Score 200.2; DB 5;
t Local Similarity 98.1%; Pred. No. 2.2e-53;
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
ery Match 10.9%; Score 200.2; DB 5;
ery foral Similarity 98.1%; Pred. No. 3.3e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS28795 standard; cDNA; 367 BP.
Human immunoglobulin encoding cDNA SEQ ID No 41.
WO200155315-A2.
                                                                                                                     ) 25-MAR-1999.
A (GETH ) GENENTECH INC.
Query Match 11.2%; Score 207; DB 2;
Best Local Similarity 99.5%; Pred. No. 1.3e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.8%; Score 198.4; DB 4 94.9%; Pred. No. 1.1e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADL38773 standard; DNA; 263 BP.
Human ovarian cancer DNA marker #12663.
WO200170979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL45157 standard; DNA; 517 BP.
Human ovarian cancer DNA marker #19047.
WO200170979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADI73644 standard; DNA; 263 BP.
Human ovarian cancer DNA marker #6386.
WO200170979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI91738 standard; cDNA; 403 BP.
Human polynucleotide SEQ ID NO 11798.
WO200164835-A2.
                                                          AAX56546 standard; DNA; 219 BP.
Human 2382718 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                       AAX56549 standard; DNA; 234 BP.
Human T39607 DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                     AAX56523 standard; DNA; 396 BP.
Human T84016 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA; 203 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX56567 standard; DNA; 203
Human 1611708 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                              25-MAR-1999.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 526
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Best Local Similarity
RESULT 527
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RESULT 528
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                 WO9914241-A2.
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ID AA1917:
DE Human PN WO2001
PD 07-SEP
PA (HYSE-)
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AAL02302 standard; cDNA; 367 BP.
Human reproductive system related antigen cDNA SEQ ID NO: 2303.
WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 10.6%; Score 195.6; DB 10; Length 367; Local Similarity 76:1%; Pred. No. 8.2e-52;
                                                                                                                                                    10.6%; Score 195.6; DB 4; Length 367; 76.1%; Pred. No. 8.2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 194.8; DB 2; Length 205; Pred. No. 1e-51;
                                                                                                                                                                                                                                                                                                                           4; Length 367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 10.4%; Score 191; DB 2; Length 191; Local Similarity 100.0%; Pred. No. 1.7e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.

ry Match 10.6%; Score 194.4; DB 2;
t Local Similarity, 93.6%; Pred. No. 1.8e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.6%; Score 195.6; DB 6; 76.1%; Pred. No. 8.2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA encoding a novel protein SEQ ID NO 41 US2003077606-A1.
                                                                                                                                                                                                                                                                                                                      10.6%; Score 195.6; DB 4 76.1%; Pred. No. 8.2e-52;
Best Local Similarity 76.1%; Pred. No. 8.2e-52; RESULT 531
                                                                                                                                                                                                                                                                                                                                                                       Human polynucleotide SEQ ID NO 324. US2002090672-A1.
                                                                                                                                                                                                                ABA06658 standard, cDNA, 367 BP. Human cDNA SEQ ID NO: 324. WO200154474-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB31520 standard; cDNA; 367 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX56501 standard; DNA; 303 BP.
Human C17760 DNA fragment.
WO9914241-A2.
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Human 1684149 DNA fragment.
WO9914241-A2.
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Human 1508552 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX56536 standard; DNA; 198 BP.
Human 1610836 DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX37717 standard; DNA; 297 BP.
Human clone 1452523 DNA.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2002.
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                  Best Local Similarity RESULT 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local_Similarity
RESULT 536
                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                             02-AUG-2003
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Query Match 9.8%; Score 179.6; DB 2; Length 201; Best Local Similarity 91.5%; Pred. No. 8.1e-47; RESULT 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QUELY MATCh 8.7%; Score 160.4; DB 2; Length 204; Best Local Similarity 99.4%; Pred. No. 1.3e-40; RESULT 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MC5-MAR-1999.
(GETH ) GENENTECH INC.
7.8%; Score 144.4; DB 2; Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vuery Match 8.6%; Score 158.4; DB 2; Length 274;
Best Local Similarity 95.9%; Pred. No. 6.6e-40;
RESULT 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.7%; Score 160.4; DB 2; Length 198; 99.4%; Pred. No. 1.2e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100.0%; Pred. No. 8.3e-43;
Best Local Similarity 100.0%; Pred. No. 8.3e-43;
BESULT 543
BESULT 543
BE Human 1889866 DNA; 203 BP.
BE Human 1889866 DNA fragment.
BP WOOSJ4241-42.
BP CS-MAR-1999.
PA (GETH ) GENENTECH INC.
           Length 297;
                                                                                                                                                            Length 186;
                                                                                               PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 6.7e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.9%; Score 163.2; DB 2. Best Local Similarity 92.7%; Pred. No. 1.6e-41; RESULT 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.3%; Score 153.4; DB 2
Best Local Similarity 84.8%; Pred. No. 2.2e-38;
RESULT 548
         10.2%; Score 187; DB 2; 83.2%; Pred. No. 4.2e-49;
                                                            AAX56591 standard; DNA; 186 BP.
Human 1208791 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX56534 standard; DNA; 204 BP.
Human 1521745 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX56516 standard; DNA; 274 BP.
Human 2861301 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX56520 standard; DNA; 198 BP.
Human T73746 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX56594 standard; DNA; 147 BP.
Human 241604 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                             AAX56543 standard; DNA; 201 BP.
Human 360948 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                               AAX56530 standard; DNA; 167 BP.
Human AA404390 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX56533 standard; DNA; 198 BP.
Human 1519947 DNA fragment.
WO9914241-A2.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 545
Query Match
Best Local Similarity
RESULT 540
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ABL97457 standard; DNA; 4067 BP.
Human testicular antigen encoding DNA fragment SEQ ID NO: 2109.
WO200155317-A2.
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WO200155317-A2.
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PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 6.8%; Score 124.4; DB 5; Length 447;

Best Local Similarity 85.2%; Pred. No. 8.1e-29;

RESULT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AALO4534 standard; DNA; 4067 BP.
Human reproductive system related antigen DNA SEQ ID NO: 7222
WO200155320-A2.
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Human reproductive system related antigen DNA SEQ ID NO: 7225
WO200155320-A2.
                                                                                                                                                                                   7.2%; Score 132.6; DB 2; Length 141; 95.7%; Pred. No. 9.1e-32;
                                                                                                                                                                                                                                                                                                                                                                                 Length 265;
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
617 MATCh
618 SCOTE 124.4; DB 5;
617 MATCh
618 SIGNIATITY 85.28; Pred. No. 5.9e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vuery Match 6.3%; Score 116; DB 12;
Best Local Similarity 100.0%; Pred. No. 6.3e-26;
RESULT 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vuery Match 6.4%; Score 118; DB 2;
Best Local Similarity 91.3%; Pred. No. 5.4e-27;
RESULT 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

QUERY MATCh 6.2%; Score 115; DB 4;

Best Local Similarity 80.5%; Pred. No. 3.3e-25;

RESULT 556
Best Local Similarity 98.6%; Pred. No. 1.5e-35; RESULT 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 6.2%; Score 115; DB 4;
Local Similarity 80.5%; Pred. No. 3.3e-25;
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HUMA-) HUMAN GENOME SCI INC.
PY MATCH 6.2%; Score 115; DB 4;
Rt Local Similarity 80.5%; Pred. No. 3.3e-25;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 85.2%; Pred. No. 5.9e-
RESULT 55.1

ID ABV12650 standard; CDNA; 447 BP.
DE Human prostate expression marker CDNA 12641.
PN W0200160866-A2.
                                                                                                                                                                                                                                                        ABV33780 standard; cDNA; 265 BP.
Human prostate expression marker cDNA 33771.
WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ67406 standard; DNA; 901 BP.
Human ovarian specific gene SEQ ID NO:120.
12-FEB-2004.
(DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL97460 standard; DNA; 4067 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX56593 standard; DNA; 180 BP.
Human 143613 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-2001, (HUMA-) HUMAN GENOME SCI INC.
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(HUMA-) HUMAN GENOME SCI INC.
                                                            AAXS6512 standard, DNA; 141
Human 2612024 DNA fragment.
WO9914241-A2.
                                                                                                                                   25-MAR-1999.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 550
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Best Local Similarity
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Length 110000;

6; Length 2522;

us-10-785-220b-11.rng.spdi

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AAK78375 standard; DNA; 6780 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33187.
WO200157182-A2.
                                           DB 6; Length 110000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 113.2; DB 9; Length 78313; Pred. No. 7.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human FYN carcinoma associated gene, SEQ ID NO:1136 WO2003057146-A2.
                                                                                                                                                     Score 113.4; DB 12;
Pred. No. 8.2e-24;
                                                                                                                                                                                                           Score 113.4; DB 12;
Pred. No. 8.2e-24;
                                                                                                                                                                                                                                                                                                                     113.4; DB 12;
No. 8.2e-24;
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Pred. No. 8.2e-24;
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No. 8.2e-24;
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Pred. No. 8.2e-24;
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cy Match

c. Local Similarity, 79.3%; Pred. No. 1.7e-24;
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                                                                                                  Score 113.4; DB 6;
Pred. No. 8.2e-24;
                                             Score 113.4; DB 6 Pred. No. 8.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.1%; Score 113.2; DB 6 76.0%; Pred. No. 9.5e-25;
                                                                                                                                                                                                                                                                                                                       Score 113.4;
Pred. No. 8.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) 27-DEC-2001.
( BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
Query Match 6.1%; Score 113.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA96879 standard; cDNA; 2522 BP.
Retinal binding site 12-encoding cDNA.
                                                                                                                                                                                                                                                                  Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ01022 standard; DNA; 56520 BP. Wild type PG1 coding sequence. W09932644-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB72356 standard; DNA; 78313 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                 6.2%;
                                                                                                                                                                                                                                                                                                                                                                          6.2%;
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                                             6.2%;
                                                                                                  6.2%;
                                                                                                                                                     6.2%;
                                                                                                                                                                                                           6.28;
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(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 576
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RESULT 578
                                                            Local Similarity
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Best Local Similarity
RESULT 574
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RESULT 581
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Best Local Similarity
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Best Local Similarity
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WOZ003008583-A2
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(GEST ) GENSET.
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                                             Match
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                            RESULT 567
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                                                                                                                       Best
                                                                                                                                                                                                                                                                                                                                    AAK78096 standard; DNA; 1498 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK81910 standard; DNA; 12466 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36722.
WQ200157182-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vuery Match 6.2%; Score 114.2; DB 4; Length 12466;
Best Local Similarity 74.1%; Pred. No. 1.2e-24;
RESULT 563
                                                                                                                                                                                    ABL37459 standard; DNA; 7633 BP.
Human testicular antigen encoding DNA fragment SEQ ID NO: 2111.
W0200155317-A2.
02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
6.2%; Score 115; DB 4; Length 7633;
St Local Similarity 80.5%; Pred. No. 4.9e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 100944;
                    RESULT 558
ID AAL04536 standard; DNA; 7633 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7224.
PN WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                 6.2%; Score 114.4; DB 4; Length 1498; 81.8%; Pred. No. 2.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3591;
                                                                                                                                 Length 7633
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Human chromosome 2p21-22 fragment containing the DRIP gene.
WO2003093310-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA198065 standard; cDNA; 3591 BP.
Human neuroblastoma expressed polynucleotide SEQ ID NO 8.
WO200166733-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADQ59368 standard; DNA; 100944 BP.
Human cancer-associated (CA) gene sequence SEQ ID NO:4.
WO2004058288-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aυγυ/266 standard; DNA; 355211 BP.
Human cancer associated sequence HD08-023, SEQ ID 242.
WO20049060304-A2.
LUNCTIVE SYSTEM related antigen DNA SE.

PD 02-ANG-201.

PA (HUMA-) HUMAN GENOME SCI INC.

QUETY MATCH 6.2%; Score 115; DB 4; Len

Best Local Similarity 80.5%; Pred. No. 4.9e-25;

ID ABL97459 standard; DNA; 7633 BP.

DE Human testicular antigen ence.

PN W0200155317-A2.

PD 02-ANG-200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 113.6; DB 10;
Pred. No. 7.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
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Pred. No. 7.9e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.2%; Score 114; DB 12; 75.9%; Pred. No. 5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
sry Match 6.2%; Score 113.6; DB 12
sry Match 74.8%; Pred. No. 7.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHISH ) CHIBA PREFECTURE.
(HISM ) HISAMITSU PHARM CO LID.
ry Match 6.2%; Score 114.4; DB 4
t Local Similarity 80.1%; Pred. No. 4.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX56595 standard; DNA; 114 BP.
Human 816576 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.2%; S
100.0%;
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(HUMA-) HUMAN GENOME SCI INC.
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(SAGR-) SAGRES DISCOVERY INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-2003.
(UYBR-) UNIV BREMEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 565
                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 566
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Best Local Similarity
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RESULT

Length 56516;

Length 6780;

Length 56520;

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RESULT 592
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Lowery Match
Best Local Similarity 78.9%; Pred. No. 1.1e-23;
RESULT 588
ID ABL66947 standard; DNA; 62944 BP.
DE Lung cancer related gene sequence pr Wo200194629-A2.
PD WO200194629-A2.
PD 13-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-2003.
(INCY-) INCYTE GENOMICS INC.
ery Match
6.1%; Score 112.6; DB 10; Length 214520;
                                                                                                                                                                                                                Length 155937;
                                                                                DB 10; Length 78313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Length 62944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A198077 standard; cDNA; 2267 BP.
Human neuroblastoma expressed polynucleotide SEQ ID NO 20.
Human neuroblastoma expressed polynucleotide SEQ ID NO 20.
HOSEP-2001.
(CHIB-) CHIBA PREFECTURE.
(HISA) HISAMITSU PHARM CO LTD.
61.1%; Score 112.6; DB 4; Length 2267;
st Local Similarity 77.4%; Pred. No. 1.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                        Human reproductive system related antigen DNA SEQ ID NO: 5533.
WO200155320-A2.
                                                                                                                                                                                                                                                                           Human reproductive system related antigen DNA SEQ ID NO: 5534 WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                             DB 4; Length 6670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 7713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 2267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA197922 standard; cDNA; 2267 BP.
Human neuroblastoma expressed polynucleotide SEQ ID NO 3997.
WO200166719-A1.
                                                                                                                              ADQ19389 standard; DNA; 155937 BP.
Human soft tissue sarcoma-upregulated DNA - SEQ ID 2208
WO2004048938-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osteoarthritis-associated polymorphic nucleotide #3 WO2003054166-A2.
                                                                                                                                                                                    PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
6.1%; Score 113.2; DB 12;
Best Local Similarity 79.3%; Pred. No. 1.2e-23;
RESULT 583
                                                                                                                                                                                                                                                                                                                                                                                                                                    G2-Aug-2001.
(HUMA-) HUMAN GENOME SCI INC.
6ry Match
6ry Match
76.6%; Pred. No. 2.5e-24;
                                                                                                                                                                                                                                                                                                   WOACCELL

02-AUG-2001.

(HUMAL) HUMAN GENOME SCI INC.

(HIMAL) 6.1%; Score 112.8; DB 4;

(ery Match

6.1%; Score 112.8; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WOZUCZ-2001.

13-5EP-2001.

(CHIB-) CHIBA PREFECTURE.

(HISM ) HISAMITSU PHARM CO LTD.

(HISM ) HISAMITSU PHARM CO LTD.

6.1%; Score 112.6; DB 4;
                                                            (SAGR-) SAGRES DISCOVERY.

ry Match 6.1%; Score 113.2; DB 1(

t Local Similarity 79.3%; Pred. No. 7.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.1%; Score 112.6; DB 6 78.9%; Pred. No. 1.1e-23;
ADE95866 standard; DNA; 78313 BP.
Human FYN gene genomic DNA sequence.
WO2003039484-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADL13471 standard; DNA; 214520 BP
                                                                                                                                                                                                                                                              AAL02846 standard; DNA; 6670 BP
                                                                                                                                                                                                                                                                                                                                                                                          AAL02845 standard; DNA; 7713 BP
                    AL-) AVALON PHARN
SIT MATCH
BEST LOCAL SIMILATITY 7.
RESULT 589
ID ADMISTATI STANGP
DE OSTEGOALTH':
PN WO20030"
PD 03-
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 585
ID A4197922 standard; cD
DE Human neuroblastoma e
PN WQ200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECT
PA (HISM ) HISAMITSU PHA
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Best Local Similarity
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Best Local Similarity
RESULT 587
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RESULT 586
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AAK82548 standard; DNA; 1118 BP.

Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37360.

WQ200157182-A2.

(HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Match 6.1%; Score 112.4; DB 10; Length 177531; Local Similarity 74.2%; Pred. No. 2.3e-23;
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1 (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

6.1%; Score 112.4; DB 10; Length 177531;

Best Local Similarity 74.2%; Pred. No. 2.3e-23;
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                                                                                                                                                                                                                                                                                                                                                     Ouery Match 6.1%; Score 112.4; DB 8; Length 177531;
Best Local Similarity 74.2%; Pred. No. 2.3e-23;
                                                                                                                                                    Length 29328
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6.1%; Score 112.2; DB 4; Length 1118;
Best Local Similarity 77.7%; Pred. No. 1.2e-24;
RESULT 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1053;
RESULT 590

ID ADR67086 standard; DNA; 29328 BP.

ID Human cancer associated gene genomic sequence SEQ ID NO:132.

PN WO2004074321-A2.

PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                                          ACF62732 standard; DNA; 177531 BP.
Cancer based on CYP3A5 related polymucleotide SEQ ID NO:660.
W02003013534-A2.
20-FEB-2003.
(EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MRP1 based cancer related nucleic acid SEQ ID NO:660.WO2003013533-A2.
                                                                                                                                        vuery Match 6.1%; Score 112.4; DB 13;
Best Local Similarity 78.3%; Pred. No. 7.7e-24;
RESULT 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vuery Match 6.1%; Score 112.2; DB 2; Beet Local Similarity 79.1%; Pred. No. 1.2e-24; RESULT 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vuery match 6.1%; Score 112.4; DB 8
Best Local Similarity 74.2%; Pred. No. 2.3e-23;
RESULT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.1%; Score 112.4; DB 1074.2%; Pred. No. 2.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human MDR1 related DNA sequence SEQ ID NO:660.
WO2003013537-A2.
20-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB92110 standard; DNA; 177531 BP.
Human MDR1 related DNA sequence SEQ ID NO:660.
WO2003013535-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADH74617 standard; DNA; 177531 BP.
Human BAC clone GS1-259H13 CYP3A5 genomic DNA.
US2003143537-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AD887936 standard; DNA; 177531 BP.
Human UGT1A1 gene sequence SEQ ID NO:660.
WO2003013536-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                               ADB20847 standard; DNA; 177531 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB96919 standard; DNA; 177531 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX30165 standard; DNA; 1053 BP.
Human secreted protein gene 21.
WO9910363-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAR-1999.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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RESULT 594
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RESULT 596
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RESULT 611
                    Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37359
WO200157182-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AN90803 standard; DNA; 1446 BP.
Breast cancer related marker, seq id 11953.
US20309974-A1.
29-MAY-2003.
(MILL-) MILLENNIUM PHARM INC.
ery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 1815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
cy Match 6.1%; Score 112.2; DB 4; Length 5281;
t Local Similarity 72.4%; Pred. No. 3.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.1%; Score 111.8; DB 12; Length 548; 98.3%; Pred. No. 1.1e-24;
                                                                                                                                                                                                                                                             Length 1815;
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8; Length 1815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.1%; Score 112.2; DB 8; Length 1815; 97.4%; Pred. No. 1.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL04261 standard; DNA; 5281 BP.
Human reproductive system related antigen DNA SEQ ID NO: 6949.
WO200155320-A2.
                                                                                                   Length 1119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACC50499 standard; cDNA; 1815 BP.
Human secreted protein coding sequence, SEQ ID 166.
WQ200295010-A2.
                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
ry Match
t Local Similarity 97.4%; Pred. No. 1.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO. 
ry Match 6.1%; Score 112.2; DB 10; t Local Similarity 78.3%; Pred. No. 7.4e-24;
                                               09-AUG-2010.
(HUMA-) HUMAN GENOME SCI INC.
6-18; Score 112.2; DB 4
6-17 Match 6.18; Pred. No. 1.2e-24;
                                                                                                                                                                                                                                                                                                                ADA39913 standard; cDNA; 1815 BP.

Human secreted protein encoding cDNA.
W02002102993-A2.
27-DEC-2002.

(HUMA) HUMAN GENOME SCI INC.
6.1%; Score 112.2; DB 8
st Local Similarity 97.4%; Pred. No. 1.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.1%; Score 112.2; DB 1097.4%; Pred. No. 1.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACH80161 standard; DNA; 548 BP.
Human genome derived single exon probe #13356.
US2003194704-Al.
                                                                                                                              Human secreted protein gene 26 SEQ ID NO:36. WO200017222-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA56101 standard; DNA; 1815 BP.
Gene encoding human secreted protein #280.
WO2002102994-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC87234 standard; DNA; 21581 BP.
Human GPCR gene SEQ ID NO:1687.
EP1270724-A2.
AAK82547 standard; DNA; 1119 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                Best Local Similarity RESULT 600
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Best Local Similarity
RESULT 607
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
RESULT 604
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  A SA SE CO
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ABK43076 standard; DNA; 32169 BP.
Genomic sequence #975 encoding novel human connective tissue polypeptide.
W0200155343-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR05591 standard; cDNA, 4865 BP.
Full length human cDNA useful for treating neurological disease Seq 97.
EP1447413-A2.
                                                                                                                                                                                                                                                                                                                                                      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 111.8; DB 11; Length 118931; Pred. No. 2.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMAN GENOME SCI INC.

ry Match HUMAN GENOME 6.1%; Score 111.8; DB 4; Length 37736;

t Local Similarity 76.5%; Pred. No. 1.4e-23;
                                                                                             02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
PLY MATCH
st Local Similarity 76.5%; Pred. No. 1.3e-23;
                                                                                                                                                                                                                                                                                         Length 32169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.0%; Score 111.4; DB 13; Length 4865; 79.8%; Pred. No. 5.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA differentially expressed in granulocytic cells #147.
WO200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 90220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 843;
                                                                                                                                                                                                                                                                                         6.1%; Score 111.8; DB 9; 76.5%; Pred. No. 1.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 6.0%; Score 111.4; DB 2; Local Similarity 58.1%; Pred. No. 8.6e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%; Score 111; DB 4;
80.1%; Pred. No. 2.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-2010.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 6.0%; Score 111; DB 5;
 76.5%; Pred. No. 1.9e-24;
                                                                                                                                                                                         ADB61232 standard; DNA; 32169 BP.
Connective tissue related genomic DNA #975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human channel/transporter gene #21
WO200154472-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO 8711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACN44586 standard; DNA; 118931 BP.
Human genomic sequence hCG30014.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA; 90220 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-AUG-2004.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                              AAK86139 standard; DNA; 37736 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA; 715 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 6.1%;
Local Similarity 75.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX56597 standard; DNA; 242
Human 951273 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-1999.
(GETH ) GENENTECH INC.
Best Local Similarity
RESULT 608
                                                                                                                                                                                                                                                                                                      Best Local Similarity
RESULT 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK83576 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM19224 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                               US2003054375-A1.
                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-200
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SOPPET D R.
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(RUBE/) I
(LIYY/) I
(ZENG/) I
(KYAW/) I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD44878 standard, cDNA, 1022 BP.
Human secreted protein-encoding gene 25 cDNA clone HTEBB42, SEQ ID NO:35.
US2002076756-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein-encoding gene 25 cDNA clone HTEEB42, SEQ ID NO:35.
US2002077287-A1.
Human junctional adhesion molecule 2 (huJAM2) coding sequence.

PW W02003008541-A2.

PD 30-JAM-2003.

PA (ELIL) LILLY & CO ELI.

Query Match

Best Local Similarity 54.0%; Pred. No. 2.6e-24;

RESULT 618

ID AAF74414 standard; DNA; 905 BP.

DE Angiogenesis protein AA1 m...

PN W0200111086-A2.

PA (FEB-200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP56686 standard; cDNA; 972 BP.
Human junction adhesion molecule 2 splice variant (huJAM2sv) cDNA,
WO2004053058-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LILLEY MATCH

BEST LOCAL SIMILARITY S4.0%; Score 111; DB 12; Length 972;

RESULT 6.1

ID AAV34310 standard; DNA; 1022 BP.

DE Human secreted protein gene 25.7

PD 17-SEP-1999

PA (FILLE PROTE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 905;
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ry Match
t Local Similarity 54.0%; Pred. No. 2.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PD 15-FEB-2001.

PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match

6.0%; Score 111; DB 5;

Best Local Similarity 54.0%; Pred. No. 2.6e-24;

RESULT 619
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54.0%; Pred. No. 2.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI61103 standard; cDNA; 930 BP.
Human polynucleotide SEQ ID NO 5092.
WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD44660 standard; cDNA; 1022 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JR/)
OUN/) YOU.
GREEN,
GREEN,
FERRIE A
LETY MATCH
JOEL LOCAL Similarity 5
DE ALIVEN RUBT
PA (RUBE) RUBT
PA (RUBE) RUBT
PA (RUBE) RUBT
PA (RUBE) RUBT
PA (RUBT)
PA 
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ZENG Z.
KYAW H.
FISCHER C L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KXAW) KXAW H.
(FISC) FISCHER C L.
(LIHH) LI H.
(SOPP) SOPPET D R.
(GENT) GENTZ R.
(WEIY) WEI Y.
(WOOR,) WOONE P A.
(YOUN) YOUNG P E.
(GRRE) GREENE J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RUBEN S M.
ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUL-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-2002.
(RUBE/) RUBE
(ROSE/) ROSE
(LIYY/) LI Y
(ZENG/) ZENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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JOHNSON Standard; DNA; 1022 BP.

Human secreted protein-related DNA - SEQ ID 349.

N W02003038063-A2.

N 96-MY-2003.

H (HUMA-) HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 54.0%; Pred. No. 2.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                         6.0%; Score 111; DB 8; Length 1022; 54.0%; Pred. No. 2.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
ry Match 6.0%; Score 111; DB 9; Length 1022;
t Local Similarity 54.0%; Pred. No. 2.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human CDNA from secreted protein gene 25. 04-DEC-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB91286 standard; cDNA; 1022 BP.
Human secreted protein cDNA #SEQ ID 232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADG89762 standard; cDNA; 1022 BP.
                                                                                                                                                                                                                                                                                                                                                                                      JOUNG P.

JOUNG P.

JOURNELL AMECH.

Best Local Similarity
RESULT 627

ID ADB91286 stand?

DE Human secr.

PN W02003^*

PD 16-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LI Y.
ZENG Z.
KYAW H.
FISCHER C L.
(GENT/) GENTZ R L.
(WEIY/) WEI Y.
(MOOR/) MOORE P A.
(YOUN/) YOUNG P E.
(GRRE/) GREENE J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 628
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RESULT 629
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Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 637
                                                                                                                                                                 Length 1022;
                                                                                                                                                                                                                                                             OJ-OCT-1998.
(GEMY) GENETICS INST INC.
ery Match
ery Match
for Store III; DB 2; Length 1076;
ery Match
for Store III; DB 2; Length 1076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1295
                                                                                                                                                                                                       AAV82780 standard; CDNA; 1076 BP.
Clone ct684 4 isolated from human adult brain CDNA library
WO9842739-AZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC58586 standard; cDNA; 1295 BP.
Human PR0245 protein UNQ219 encoding cDNA SEQ ID NO:35.
WO200053758-A2.
14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX81770 standard; cDNA; 1295 BP.
cDNA DNA35638 encoding A33 related antigen PRO245.
WO9927098-A2.
                                                                                                                                                    Best Local Similarity 54.0%; Pred. No. 2.8e-24; RESULT 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.0%; Score 111; DB 2; Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.0%; Score 111; DB 6; 54.0%; Pred. No. 2.9e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AASOO512 standard; cDNA; 1131 BP.
Human junctional adhesion protein (JAM2) cDNA.
WO200114404-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX52225 standard; DNA; 1295 BP.
Protein PRO245 cDNA clone DNA35638-1141.
WO9914328-A2.
                                                                                                                                                                                                                                                                                                                                           Human polynucleotide SEQ ID NO 14.
US2002055394-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001.
(TEXA-) TEXAS BIOTECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX37664 standard; cDNA; 1295 BP. Human PRO245 cDNA. W09914241-A2. 25-MAR-1999. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                             MCCOY J M.
LAVALLIE E R.
COLLINS-RACIE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUN-1999.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-1999.
(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MERB/) MERBERG D.
(TREA/) TREACY M.
(SPAU/) SPAULDING V.
                                                                                                                                               HASTINGS G A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 632
                                                                        (MOOR/) MOORE P A.
(YOUN/) YOUNG P E.
(GREE/) GREENE J M.
(FERR/) FERRIE A M.
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 633
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                                         GENTZ R L.
                                                                                                                                                                                                                                                                                                                                                                                                                              JACOBS K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVANS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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AAC97437 standard, cDNA, 1295 BP.
Human anglogenesis-associated protein PRO245 cDNA, SEQ ID NO:90.
WO200053753-A2.
                                                                23-MAR-2000.
(GETH) GENENTECH INC.
STY MATCH 6.0%; Score 111; DB 3; Length 1295; t Local Similarity 54.0%; Pred. No. 3.2e-24;
                                                                                                                                                                                                                                                                               Length 1295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AASO0157 standard; cDNA; 1295 BP.
Human cDNA clone DNA35638-1141 encoding PRO245 (UNQ219)
WO200119991-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAĞ0052 standard; cDNA; 1295 BP.
Human cDNA for secreted/transmembrane protein PRO245.
US2003003530-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA sequence encoding for PRO245 polypeptide WO200140466-A2.
                                                                                                                                                                                                                                       08-JUN-2000.
(GETH ) GENENTECH INC.
6.0%; Score 111; DB 3;
rry Match 6.0%; Pred. No. 3.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.0%; Score 111; DB 4;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.0%; Score 111; DB 4;
54.0%; Pred. No. 3.2e-24;
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Local Similarity 54.0%; Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 645
AAZ52202 standard; cDNA; 1295 BP.
Human PRO245 protein encoding cDNA, UNQ219.
WO200015797-A2.
                                                                                                                                                                     AAA77562 standard, cDNa, 1295 BP.
Human PR0245 cDNa sequence SEQ ID NO:66.
W200032221-A2.
08-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC91463 standard; cDNA; 1295 BP.
Human PRO245 cDNA.
WO200073452-A2.
                                                                                                                                                                                                                                                                                                                                           ADC78383 standard; cDNA; 1295 BP. Human PRO245 cDNA. WO200015796-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF72383 standard; cDNA; 1295 BP.
Human PRO245 cDNA.
WO200104311-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS21411 standard; cDNA; 1295 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .02-JAN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JAN-2001.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 643
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Best Local Similarity
RESULT 644
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ABX89308 standard; cDNA; 1295 BP.
DNA encoding novel secreted and transmembrane protein PRO245.
US2003017563-A1.
                                                                                                                     Length 1295;
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              ACD07452 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2002197571-A1.
26-DEC-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                           ABX71500 standard; cDNA; 1295 BP.
Human cDNA encoding secreted/transmembrane protein PRO245.
US2002132240-A1.
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ID ACD20057 standard; CDNA; 1295 BP.

DE Human secreted / transmembrane polypeptide PRO245 CDNA. BP. U3200303606-A1.

PD 20-FEB-2003.

PA (GETH ) GENENTECH INC.
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Human secreted/transmembrane protein (PRO) cDNA #168.
US200303619-A1.
20-FEB-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACHOG6832 standard; cDNA; 1295 BP.
Human secreted/transmembrane polypeptide PRO245 cDNA.
US2003044839-A1.
                                                                                                                 Query Match
Best Local Similarity 54.0%; Score 111; DB 8;
RESULT 647.0%; Pred. No. 3.2e-24;
RESULT 647.00 standard; cDNA; 1295 BP.
DE CDNA encoding human PRO polypeptide #168.
PD 105209305180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 650
DE ABX9308 standard; CDNA, 1295 BP.
DE DNA encoding novel secreted and transmembrane pp. Ny2003017563-A1.
Pp. 23-JAN-2003.
Pp. GETH ) GENENTECH INC.
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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cDNA encoding human secreted protein PRO245.
US2003023054-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity 5
RESULT 61
ID ACD41962 standard; CDN
DE Human secreted/transme
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
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RESULT 652
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Best Local Similarity
RESULT 649
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RESULT 655
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RESULT 646
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Human cDNA encoding a secreted/transmembrane protein, SEQ ID 335. US2003032155-A1.
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US2003092002-A1.
15-MAY-2003.
(GETH ) GENENTECH INC.
6.0%; Score 111; DB 9; Length 1295; St Local Similarity 54.0%; Pred. No. 3.2e-24;
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06-FEB-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                ACAS4860 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245
US2003017463-A1.
33-JAN-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO245
US2003022328-Al.
ABX93348 standard; cDNA; 1295 BP.
cDNA encoding human A-33 related antigen PRO245.
US20022206-A1.
05-DEC-2002.
(GETH ) GENENTECH INC.
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                                                                                                 Score 111; DB 8;
Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA18935 standard; cDNA; 1295 BP. Human PRO polynucleotide #168. 20.082003054517-A1. 20-MAR-2003. (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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L2003.
LETH ) GENENTECH LEGEL LOCAL SIMILARITY RESULT 661

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DE Human secrer
PN US20030°
PD 15-**
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                                                                                                                 Best Local Similarity
RESULT 656
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                                                                                                                                                           ACA04191 standard;
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US2003049816-A1.
                                                                                                   Query Match
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US2003082693-A1.
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(GETH ) GEN
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(GETH ) GEN
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                                                                            Length 1295;
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Novel human secreted and transmembrane protein PRO245 cDNA.
122003068795-A1.
10-ARR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                ADA86363 standard; cDNA; 1295 BP. Novel human secreted and transmembrane protein PRO245 cDNA, US200308211-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 666
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Pred. No. 3.2e-24;
                                                                          6.0%; Score 111; DB 9; 54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 667
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54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 672
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Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13.
US2003039971-A1.
                                                                                                                              ADB27884 standard; cDNA; 1295 BP.
cDNA encoding human PRO polypeptide #168.
US2003082704-A1.
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CONA encoding human PRO polypeptide #168.
US2003068794-A1.
10-APR-2003.
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Human PRO polynucleotide #168.
US2003087350-Al.
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Human PRO polynucleotide #168.
US2003073215-A1.
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Human PRO polynucleotide #168.
US2003068795-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 668
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Best Local Similarity
                                                                                      Best Local Similarity RESULT 665
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                                                                            Match
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                                                                            Query
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Length 1295;
                                                                                                                                                                                  Match 6.0%; Score 111; DB 9; Length 1295; Local Similarity 54.0%; Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087345-A1.
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Novel human secreted and transmembrane protein PRO245 CDNA.
US2003073211-A1.
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                 6.0%; Score 111; DB 9;
54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Local Similarity 54.0%; Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13
US2003049621-A1.
                                                                       Human PRO polynucleotide #168.
01-MAV.200.
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Human PRO polynucleotide #11.
US2003044793-A1.
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Human PRO polynucleotide #168.
US2003082763-A1.
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Human PRO polynucleotide #168.
US2003087351-A1.
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01-MAY-2003.
(GETH ) GENENTECH INC.
4.0%; SC
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US2003087349-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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GENENTECH INC.
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                   Query Match
Best Local Similarity
RESULT 674
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(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003082691-A1.
01-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                             ACD98591 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003044945-A1.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 687

DE ADA-461 standard; CDNA, 1295 BP.
PN US2003068798-Al.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
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                        Ouery Match 6.0%; Score 111; DB 9; Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 683
                                                                                                                                             6.0%; Score 111; DB 9; 54.0%; Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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Human PRO polynucleotide SEQ ID NO 335.
US2003077713-A1.
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US2003082701-A1.
                                                                  ADA93999 standard; cDNA; 1295 BP.
Human PRO polynucleotide #168.
US-2003077722-A1.
24-APR-2003.
(GETH ) GENENTECH INC.
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Human PRO polynucleotide #168.
US2003082710-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
17-APR-2003.
(GETH ) GENENTECH INC.
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24 ) GENENTECH I.
27 MATCh
Best Local Similarity S
RESULT 685
ID ADB13207 standa
DE Human PRO r
PP US2030.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 690
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RESULT 686
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vuery Match
     6.0%; Score 111; DB 9; Length 1295;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 695
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 697
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 698
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   Length 1295;
                                                                                                                                                     Length 1295,
                                                                                                                                                                                                        ADA84707 standard; cDNA; 1295 BP. Novel human secreted and transmembrane protein PRO245 cDNA. US2003082708-A1.
                                                      ADA85259 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA
US2003082695-A1.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 699
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PA (GETH) GENENTECH INC.
QUERY MATCh
BEST Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 693
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 696
6.0%; Score 111; DB 9;
54.0%; Pred. No. 3.2e-24;
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cDNA encoding human PRO polypeptide #168.
US2003073214-A1.
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Human PRO polynucleotide SEQ ID NO 335.
US2003077715-A1.
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US2003082761-A1.
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US2003073210-A1.
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Human PRO polynucleotide #11.
US2003064367-A1.
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Human PRO polynucleotide #168.
US2003077721-A1.
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Human PRO polynucleotide #168.
US2003082703-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
   Query Match
Best Local Similarity
RESULT 692
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Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 710

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ADB21713 standard; CDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 CDNA.
US2003082765-A1.
(GETH ) GENENTECH INC.
6.0%; Score 111; DB 9; Length 1295;
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                                                                     Length 1295;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 705
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 707
                                                                   6.0%; Score 111; DB 9;
54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 709
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CDNA encoding human PRO polypeptide #168.
US2003096386-A1.
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cDNA encoding human PRO polypeptide #168.
US2003082760-A1.
                                                                                                                                              cDNA encoding human PRO polypeptide #168.
US2003092147-A1.
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ID ADB24142 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335. PN US2003077714-A1.
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Homo sapiens.
US2003049817-A1.
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Human PRO polynucleotide #168.
US2003082690-A1.
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Human PRO polynucleotide #168.
US2003082702-A1.
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Human PRO polynucleotide #168.
US2003082759-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
Lry Match
Best Local Similarity the RESULT 701
ID ADB26780 stander
DE CDNA encod*
PN US2003**
PD 15-***
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(GETH ) GENENTECH INC.
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Best Local Similarity
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Best Local Similarity
RESULT 702
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Query Match 6.0%; Score 111; DB 9; Length 1295; Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 CDNA.
US2003082709-A1.
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Novel human secreted and transmembrane protein PRO245 CDNA.
01-1030.02020.
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Novel human secreted and transmembrane protein PRO245 CDNA.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 715
                                                                                                                                                                                                                                                       6.0%; Score 111; DB 9;
54.0%; Pred. No. 3.2e-24;
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US2003039969-A1.
                                                                                                                                                                            cDNA encoding human PRO polypeptide #168.
US2003077710-A1.
ADA77492 standard, cDNA; 1295 BP.
Human PRO polynucleotide #168.
US2003068797-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 712
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Length 1295;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087344-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003073213-A1.
                                                                                                                               Query Match
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 720
DE ADBESH36 standard; CDNA, 1295 BP.
DE CDNA encoding human PRO polypeptide #168.
PD 01-MAY-2003.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 54.0%; Score 111; DB 9;
RESULT 724
DE ADA91575 standard; CDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PP 01-MAY-2003.
PP 01-MAY-2003.
PP GETH ) GENENTECH INC.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 721
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 722
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 723
DE ADABS570 standard; CDNA; 1295 BP.
DN Novel human secreted and transmembrane protein FP 17-APR-2003.
PP 17-APR-2003.
PP (GETH ) GENENTECH INC.
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54.0%; Pred. No. 3.2e-24;
LT 719
ADA42670 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13.
US2003054351-A1.
20-MAR-2003.
(GETH ) GENENTECH INC.
6 0*: Score 111; DB 9;
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US2003082706-A1.
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US2003022239-A1.
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Human PRO polynucleotide #168.
US2003059909-A1.
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Human PRO polynucleotide #11.
US2003064923-A1.
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Human PRO polynucleotide #168.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 726
ID ADB22265 standard; CD
DE Novel human secreted
PN US2003087344-A1.
PD 08-MAY-2003.
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RESULT 725
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Best Local Similarity
RESULT 728
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RESULT 727
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vuery Match
Best Local Similarity 54.0%; Score 111; DB 10; Length 1295;
RESULT 736
ID ADB89627 standard; CDNA; 1295 BP.
DE Human PRO polynucleotide #168
PN US2003082698-A1.
PN US2003082698-A1.
uery Match
6.0%; Score 111; DB 9; Length 1295;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 729
ID ADB22817 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168
PN US2003077711-A1.
PD 24-APR-2007
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA.
012003082766-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087347-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003082712-Al.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 731
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 734
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Human PRO polynucleotide SEQ ID NO 335.
US2003077712-A1.
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ID ADB15375 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
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Human PRO polynucleotide #168.
US2003082762-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 730
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Length 1295;

Length 1295;

Length 1295;

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6.0%; Score 111; DB 10; Length 1295; 54.0%; Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 CDNA, US203082622-A1.
                     Score 111; DB 10;
Pred. No. 3,2e-24;
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Best Local Similarity' 54.0%; Pred. No. 3.2e-24;
RESULT 750
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13.
US20030360161-A1.
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US2003049676-A1.
13-MAR-2003.
GETH ) GENENTECH INC.
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                                                                          ADB35004 standard; cDNA; 1295 BP.
Human PRO polynucleotide SEQ ID NO 335.
US2003077718-Al.
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Human PRO polynucleotide SEQ ID NO 335.
US2003077720-A1.
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Query Match
Best Local Similarity 54.0%;
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RESULT 753
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Local Similarity 54.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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   (GETH ) GENENTECH INC.
                                 Best Local Similarity RESULT 747
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Best Local Similarity
RESULT 752
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003082687-Al.
                                                                                                                                                                                                                            Aubsy460 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
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Novel human secreted and transmembrane protein PRO245 CDNA.
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Beet Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 743
                               Query Match
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 738
                                                                                                                                                                                                                                                                                                                                          6.0%; Score 111; DB 10; 54.0%; Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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                                                                                                         Human secreted/transmembrane protein cDNA, #13
US2003077654-A1.
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Human PRO polynucleotide SEQ ID NO 335.
US2003077717-Al.
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Human PRO polynucleotide SEQ ID NO 335.
US2003077716-Al.
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Human PRO polynucleotide #168.
US2003082697-A1.
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                                                                                           ADB77589 standard; cDNA; 1295
01-MAY-2003.
(GETH ) GENENTECH INC.
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Best Local Similarity
:SULT 741
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RESULT 740
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RESULT

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Length 1295;

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ADC52909 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein cDNA Seq ID335.
US2003087365-A1.
                                                      6.0%; Score 111; DB 10; Length 1295; 54.0%; Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003092106-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003092105-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003092107-A1.
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Best Local Similarity 54.0%; Score 111; DB 10; Len
RESULT 762
ID ADC71923 standard; CDNA; 1295 BP.
DE Novel human secreted and transparents of the process of t
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13.
US2003054400-A1.
(GETH ) GENENTECH INC.
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Human secreted/transmembrane protein cDNA, #13.
US2003054441-A1.
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US2003049677-A1.
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Human secreted/transmembrane protein cDNA, #13.
US2003073077-A1.
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Human secreted/transmembrane protein cDNA, #13.
US2003073079-A1.
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(GETH ) GENENTECH INC.
6.0%; Score 111;
                                                                                                                                       ADC28795 standard; cDNA; 1295 BP.
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Best Local Similarity 54.0%; Pi
RESULT 758
ID ADC1937 standard; cDNA; 1295 E
DE Human secreted/transmembrane pi
PN US200305441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 756
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RESULT 759
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Best Local Similarity
RESULT 761
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Best Local Similarity
RESULT 757
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Best Local Similarity
RESULT 764
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AUCS/263 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein cDNA Seq ID335.
US2003087366-Al.
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Novel human secreted and transmembrane protein cDNA Seq ID335.
US2003087359-A1.
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Novel human secreted and transmembrane protein cDNA Seg ID335.
US2003087363-A1.
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US2003087364-A1.
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Novel human secreted and transmembrane protein cDNA Seq ID335.
US2003087360-A1.
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US2003087346-A1.
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Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA.
22003087367-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087361-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       111; DB 10;
No. 3.2e-24;
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(GETH) GENENTECH INC.

(GET) Match

6.0%; Score 111; DB 10;

(GET) Match

6.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 765
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Best Local Similarity 54.0%; Pred.
RESULT 768
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Human PRO polynucleotide #168.
US2003087362-A1.
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(GETH ) GENENTECH INC.
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Local Similarity 54.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                       Socal Similarity
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RESULT 769
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Best Local Similarity
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Best Local Si
RESULT 772
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RESULT 766
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ADC47908 standard; cDNA; 1295 BP.
                  Human PRO polynucleotide #168
US2003194771-A1.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 792
                                                                                                                 Length 1295;
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                                                                                                                                                             ADD03160 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003092104-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087348-A1.
08-MAY-2003.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087354-A1.
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Novel human secreted and transmembrane protein PRO245 CDNA.
125003092113-A1.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 780
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Pred. No. 3.2e-24;
    ADC12307 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13.
US2003082541-A1.
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cDNA encoding human PRO polypeptide #168.
US2003194770-A1.
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Human PRO polynucleotide #168.
US2003194773-A1.
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Human PRO polynucleotide #168.
US2003194776-A1.
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Best Local Similarity 54.0%;
RESULT 775
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 783
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RESULT 781
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RESULT 774
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Length 1295;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087358-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA
US2003203438-A1.
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PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 786
                                  Query Match 6.0%; Score 111; DB 10;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 784
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13.
US2003104381-A1.
                                                                                     ADD04862 standard; cDNa; 1295 BP.
Human secreted/transmembrane protein cDNA, #13.
US2003104469-A1.
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Human secreted/transmembrane protein cDNA, #13
US2003108983-A1.
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US2003194769-A1.
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ADD52289 standard; cDNA; 1295 BP
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05-JUN-2003.
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RESULT 792
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US2003199056-A1.
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ID ADD54152 standard; CDNA; 1295 BP.
DE Novel human secreted and transmer.
PN US2003203432-A1.
PA ADS 30-OCT-2007
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Novel human secreted and transmembrane protein PRO245 cDNA. US2003194765-Al.
     Novel human secreted and transmembrane protein PRO245 cDNA
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Best Local Similarity 54.0%; Score 111; DB 10;
RESULT 798
ELICAL ADD91365 standard; CDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PP 23-0CT-2003.
PP GETH ) GENENTECH INC.
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Pred. No. 3.2e-24;
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CDNA encoding human PRO polypeptide #168.
US2003194779-A1.
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RESULT 800
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RESULT 801
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30-OCT-2003.
(GETH ) GENENTECH INC.
(ery Match imilarity 54.0%; Score 111; DB 10; Length 1295;
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                                     6.0%; Score 111; DB 10; Length 1295; 54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 810
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Pred. No. 3.2e-24;
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Local Similarity 54.0%; Pred. No. 3.2e-24;
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US2003207417-A1.
                                                                                                                    cDNA encoding human PRO polypeptide #168 US2003203428-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                  ADE17785 standard; cDNA; 1295 BP.
Human PRO polynucleotide #168.
US2003199023-A1.
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Human PRO polynucleotide #168.
US2003199025-A1.
                                                                                                                                                                                                                                                          ADE41968 standard; cDNA; 1295 BP.
Human PRO polynucleotide #168.
US2003194772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD91917 standard, cDNA, 1295 BP.
Human PRO polynucleotide #168.
US2003199053-A1.
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                                                                                                  ADD79432 standard; cDNA; 1295 BP
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Best Local Similarity 54.0%;
RESULT 807
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                    Best Local Similarity
RESULT 802
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RESULT 803
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RESULT 806
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16-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity 54.0%; Score 111; DB 10; Length 1295;
RESULT 817
ID ADE32828 standard; cDNA, 1295 BP.
DE Novel human secreted and transmer by US2003194766-A1.
PD 16-OCT-2002
                                 6.0%; Score 111; DB 10; Length 1295; 54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 813
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 814
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Beet Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 816
                                                                                                                                                                  Query Match
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.0%; Score 111; DB 10; 54.0%; Pred. No. 3.2e-24;
                                                                                 ADE34696 standard; cDNA; 1295 BP.
Human secreted/Lransmembrane protein cDNA, #13.
US2003077583-A1.
(GETH ) GENENTECH INC.
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US2003207418-A1.
06-NOV-2003.
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cDNA encoding human PRO polypeptide #168.
US2003199064-A1.
                                                                                                                                                                                                                  ADE43085 standard; cDNA; 1295 BP.
Human PRO polymucleotide #168.
US2001199033-A1.
23-OCT-2003.
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Human PRO polynuclectide #168.
US2003199059-A1.
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Human PRO polynuclectide #168.
US2003199032-A1.
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(GETH ) GENENTECH INC.
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                                          Best Local Similarity RESULT 811
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Best Local Similarity
RESULT 815
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23-OCT-2003
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vuery Match 6.0%; Score 111, DB 10; Length 1295;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 820
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Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207384-Ai.
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Novel human secreted and transmembrane protein PRO245 cDNA
US2003207355-A1.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 821
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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ry Match
t Local Similarity 54.0%; Pred. No. 3.2e-24;
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Human PRO polynucleotide #168.
US2003199031-Al.
                                                                                                   ADD89564 standard; cDNA; 1295 BP.
Human PRO polynucleotide #168.
US2003199028-A1.
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Human PRO polynucleotide #168.
US2003199034-A1.
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Human PRO polynucleotide #168.
US2003194777-A1.
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Human PRO polynucleotide #168.
US2003207370-A1.
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Human PRO polynucleotide #168.
US2003207373-A1.
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RESULT 824
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6.0%; Score 111; DB 10; Length 1295; 54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207381-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207379-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207385-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207386-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA
US2003207387-A1.
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Human secreted/transmembrane protein cDNA, #13.
                                                                                                                                                                                                                                                                                                                                       Human secreted/transmembrane protein cDNA, #13.
US2003039972-A1.
                                                                         Human DNA35638 cDNA encoding PRO245 protein. US2003171568-A1.
                                                                                                                                                                                                                                                                                                                        ADH59179 standard; cDNA; 1295 BP.
                                                        ADH62535 standard; cDNA; 1295 BP
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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20-MAR-2003.
(GETH ) GENENTECH INC.
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Best Local Similarity 5
RESULT 811
ID ADH55265 standard, CDN
DE Novel human secreted 6
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
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                                                                                                                          (ASHK) ASHKENAZI A.
(FONG/) FONG S.
(GODD/) GODDARD A.
(GURN/) GURNEY A L.
(NAPI/) NAPIER M A.
(TUMA/) TUMAS D.
(WOOD/) WOOD W I.
Query Match
Best Local Similarity
BESULT 8.29
ID ADH62535 standard; cD
DE Human DNA35638 cDNA e
PN US2003171568-A1.
PN (L-SEP-2003.
PA (RAHK/) ASHKENAZI A.
PA (GODD/) GODDARD A.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAC)/ TUNAX D.
PA (TUNA/) TUNAS D.
PA (WOOD/) WOOD W I.
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Best Local Similarity
RESULT 837
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RESULT 830
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(GETH ) GEN
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Length 1295;
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Novel human secreted and transmembrane protein PRO245 CDNA.
13-pen 2012.
ADH81898 standard; cDNA; 1295 BP. Novel human secreted and transmembrane protein PRO245 cDNA. US2003207388-A1.
                                                                                                                                                              ADH81346 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA
US2003207377-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA
US2003087355-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087353-Al.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 840
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(GETH) GENENTECH INC.
6.0%; Score 111; DB 10;
Query Match
7:2112114 54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 841
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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                                                                                                    Score 111; DB 10;
Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACA67161 standard; cDNA; 1295 BP.
CDNA encoding human PRO polypeptide #168.
02-JAN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAS8345 standard; cDNA; 1295 BP.
cDNA encoding human PRO polypeptide #11.
US2002192659-A1.
                                                                                                                                                                                                                                                                                                                              ACA58948 standard; cDNA; 1295 BP.
Human PRO polynucleotide #11.
US2002146709-A1.
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                                                                                                    6.0%;
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RESULT 844
                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2002.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Query Match
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RESULT 845
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Best Local Si
RESULT 838
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RESULT 842
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13-NOV-2003.
(GETH ) GENENTECH INC.
      US2003211571-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087385-A1.
                                                                                                                                     ADN15362 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087356-A1.
                                                                                                                                                                                                                                                                                            ADN14810 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087357-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003092115-A1.
                                                                                                                                                                                                                                     Score 111; DB 11;
Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 854
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Pred. No. 3.2e-24;
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                                                                              6.0%; Score 111; DB 11; 54.0%; Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13.
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Human secreted/transmembrane protein cDNA, #13.
US2003130489-A1.
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US2002032440-A1.
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Human PRO polynucleotide #168.
US2003092113-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADD76520 standard; cDNA; 1295 BP.
Human PRO polynucleotide #168.
US2003100087-A1.
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Human PRO polynucleotide #168.
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Best Local Similarity 54.0%;
RESULT 848
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RESULT 849
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                Query Match
Best Local Similarity
RESULT 847
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RESULT 852
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                                          08-MAY-2003
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6.0%; Score 111; DB 12; Length 1295; 54.0%; Pred. No. 3.2e-24;
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(GETH ) GENENTECH INC.
sry Match

'Trans Similarity 54.0%; Pred. No. 3.2e-24;
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Local Similarity 54.0%; Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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Local Similarity 54.0%; Pred. No. 3.2e-24;
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Local Similarity 54.0%; Pred. No. 3.2e-24;
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                                                                            Human secreted/transmembrane protein cDNA, #13
US2003129592-A1.
                                                                                                                                                                                                                                          cDNA encoding human PRO polypeptide #168.
US2003092108-A1.
                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding human PRO polypeptide #168.
US2003092110-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE24507 standard; cDNA; 1295 BP.
cDNA encoding human PRO polypeptide #168.
US2003092111-A1.
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US2003203439-A1.
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Human PRO polynucleotide #168.
US2003199054-A1.
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Human PRO polynucleotide #168.
US2003199062-A1.
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Human PRO polynucleotide #168.
US2003194794-A1.
                                                           CDNA; 1295 BP
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 858
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                   Best Local Similarity
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                                                         ADE73241 standard;
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(GETH ) GENENTECH INC.
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                                  Score 111; DB 12; Length 1295; Pred. No. 3.2e-24;
                                                                                                                                                                                                                                                                                                                                6.0%; Score 111; DB 12; Length 1295; 54.0%; Pred. No. 3.2e-24;
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Beet Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 873
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003199051-Al.
                                                                                                                                                                            Query March
Best Local Similarity 54.0%; Score 111; DB 12;
RESULT 866
CDNA encoding human PRO polypeptide #168.
PD 23-007-2093.
PD 34-007-2003.
PD GENEWIECH INC.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 869
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 870
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 872
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                                                                                      ADE99330 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13.
US2003211576-A1.
(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE95218 standard; cDNA; 1295 BP.
cDNA encoding human PRO polypeptide #168.
US2003199052-A1.
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828003199029-A1.
23-0CT-2003.
(GETH ) GENENTECH INC.
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Human PRO polynucleotide #168.
US2003199060-A1.
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                                                                                                                                                                                                                                                                                                                                                                                    ADE91077 standard; CDNA; 1295
Human PRO polynucleotide #168.
US2003199061-A1.
23-OCT-2003.
(GETH ) GENENTECH INC.
                                  Query Match 6.0%;
Best Local Similarity 54.0%;
RESULT 865
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(GETH ) GENENTECH INC.
23-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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2003.
2.7 A1.
2.67 GENENTECH I.
2.7 Match
Best Local Similarity b
RESULT 867
ID ADE91077 standa
DE Human PRO r
PN US20031
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(GETH ) GENENTECH INC.
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Query Match 6.0%; Score 111; DB 12; Length 1295; Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 880
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Length 1295,
                                                                                Novel human secreted and transmembrane protein PRO245 cDNA US2003199058-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207360-Al.
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PA (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 54.0%; Pred. No. 3.2e-24;

RESULT 978
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(GETH) GENENTECH INC.
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st Local Similarity 54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 875
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Pred. No. 3.2e-24;
6.0%; Score 111; DB 12;
54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13.
US2003225253-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADF73740 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13.
US2003180312-A1.
                                                                                                                                                                                                                           ADE98876 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13
US2003211568-A1.
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cDNA encoding human PRO polypeptide #168.
US2003207376-A1.
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Human PRO polynucleotide #168.
US2003207352-A1.
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                                                            ADE91672 standard; cDNA; 1295 BP
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US2003207422-A1.
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RESULT 879
                                                                                                                         23-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 881
Query Match
Best Local Similarity
RESULT 874
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ADG08341 standard; cDNA; 1295 BP.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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               ADG24230 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207426-Al.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 888
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                                                                                             udery Match 6.0%; Score 111; DB 12;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 883
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54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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cDNA encoding human PRO polypeptide #168.
US2003207359-A1.
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cDNA encoding human PRO polypeptide #168.
US2003207357-A1.
                                                                                                                                                           ADF98584 standard; cDNa; 1295 BP.
Human PRO polynucleotide #168.
US2003208055-A1.
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Human PRO polynucleotide #168.
US2003207353-A1.
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Human PRO polynucleotide #168.
US2003207375-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 891
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Best Local Similarity
RESULT 890
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Best Local Similarity
RESULT 886
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Best Local Similarity
RESULT 887
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RESULT 882
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Length 1295;
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Novel human secreted and transmembrane protein PRO245 cDNA. US2003207424-A1.
US2003207424-A1.
US2003207424-A1.
(GETH ) GENENTECH INC.
6.0%; Score 111; DB 12; Length 129 of Local Similarity 54.0%; Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA. US2003207350-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207389-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207427-A1.
06-NOV-2003.
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Novel human secreted and transmembrane protein PRO245 CDNA.
US2003207356-Al.
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Local Similarity, 54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
                                                                                                                                   CDNA encoding human PRO polypeptide #168.
US2003219885-A1.
                                                                                                                                                                                                                                                                                                                        ADF96909 standard; cDNA; 1295 BP.
Human PRO polynucleotide #168.
US2003207371-A1.
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Human PRO polynucleotide #168.
US2003207374-A1.
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Human PRO polynucleotide #168.
US2003207423-A1.
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Local Similarity 54.0%;
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Local Similarity 54.0%;
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US2003207420-A1.
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RESULT 911
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Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207428-A1.
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Novel human secreted and transmembrane protein PRO245 CDNA.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207365-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA, US2003207368-A1.
06-NOV-2003.
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Novel human secreted and transmembrane protein PRO245 cDNA.
Novel human secreted and transmembrane protein PRO245 cDNA. US2003194778-A1.
                                                                                                                                    ADG60876 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA
US2003207390-A1.
                                                                            6.0%; Score 111; DB 12; 54.0%; Pred. No. 3.2e-24;
                                                                                                                                                                                                                                6.0%; Score 111; DB 12;
54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 904
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6.0%; Score 111; DB 12;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 907
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Human secreted/transmembrane protein cDNA, #13.
US2003027145-A1.
(GETB-22003.
(GETH ) GENENTECH INC.
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Human PRO polynucleotide #168.
US2003207358-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 906
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Best Local Similarity
RESULT 903
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RESULT 909
ID ADG70890 standard;
DE Novel human secrete
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RESULT 902
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(GETH ) GEN
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Length 1295;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207416-Al.
06-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADG71442 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207421-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207419-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207414-Al.
                                                                                                                                                                                                                                                                                                                                                                                                 ADG53556 standard, cDNA, 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207415-A1.
                                                                                                                                                                                                                                              ADG57972 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA
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Beet Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 915
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(GETH ) GENENTECH INC.
PTY MATCH 6.0%; SCOTE 111; DB 12;
St Local Similarity 54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
                                                                                                              Human secreted/transmembrane protein cDNA, #13 US2003027146-A1.
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US2003077723-Al.
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                                                                        RESULT 910
ID ADG92586 standard; cDNA; 1295 BP
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(GETH) GENENTECH INC.
rry Match 6.0%;
tt Local Similarity 54.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 916
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RESULT 917
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Length 1295;

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Novel human secreted and transmembrane protein PRO245 cDNA. US2004009548-A1.
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Local Similarity 54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13.
US2003148419-A1.
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Human secreted/transmembrane protein cDNA, #13.
US2003096340-A1.
                                                                                                                                                                                                Human secreted/transmembrane protein cDNA, #13 US2003215904-A1.
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US2004005665-Al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding human PRO polypeptide #168.
US2003207361-A1.
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                (GODO/) GODOWSKI P J. (GURN/) GURNEY A L. (MATH) MATHER J P. (MILL/) WILLIAMS P M. (WOOD/) WOOD W I.
                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (GODD/) GODDARD A.
(GODO/) GODOWSKI P J.
(GURN/) GURNEY A L.
(MATH/) MATHER J P.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
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RESULT 932
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    GODDARD A.
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                    Length 1295;
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Novel human secreted and transmembrane protein PRO245 cDNA.
022003207378-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207429-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207367-A1.
                                                                                                                                                                                                                                   ADG56316 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA
US2003207366-A1;
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Novel human secreted and transmembrane protein PRO245 CDNA
022003207369-A1.
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Best Local Similarity 54.0%; Score 111; DB 12; Lest RESULT 95.0%; Pred. No. 3.2e-24; LD ADH20375 standard; CDNA; 1295 BP.

PD Human secreted/transmembrance Pp US200400553-A1.

PD 08-JAN-200.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 925
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 922
                                                                                                                                                             Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 920
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
                  6.0%; Score 111; DB 12; 54.0%; Pred. No. 3.2e-24;
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US2004006211-A1.
08-JAN-2004.
                                                                          ADG81077 standard, cDNA, 1295 BP.
Human PRO polynucleotide #168.
US2003194793-A1.
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Human PRO polynucleotide #168.
US2003022331-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 927
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                Query Match
Best Local Similarity
RESULT 919
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RESULT 921 ID ADH12: DE NOVE1 PN US200: PD 06-NOV

22262

Length 1295;

Length 1295;

Length 1295;

Length 1295;

Length 1295;

Query Match

Length 1295;

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Query Match 6.0%; Score 111; DB 12; Length 1295; Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 948
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                                      6.0%; Score 111; DB 12; Length 1295; 54.0%; Pred. No. 3.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1295;
                                                                                                                                                                                              Length 1295;
                                                                                                                                                                                                                                                   AD063546 standard; cDNA; 1295 BP. Novel human secreted and transmembrane protein PRO245 CDNA. US2004039164-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vuery Match 6.0%; Score 111; DB 12;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 950
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Pred. No. 3.2e-24;
                                                                                                                                                                                                                                                                                                                                                 Query Match 6.0%; Score 111; DB 12; Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 6.0%; Score 111; DB 12;
Local Similarity 54.0%; Pred. No. 3.2e-24;
                                                                                                                                                      PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.

QUERY MAtch

6.0%; Score 111; DB 12;

Best Local Similarity 54.0%; Pred. No. 3.2e-24;

RESULT 945
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Local Similarity 54.0%; Pred. No. 3.2e-24;
                                                                                                               Human secreted/transmembrane protein cDNA, #13 US2003096233-A1.
                                                                                                                                                                                                                                                                                                                                                                                                            ADM29776 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13
US2003190611-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM27699 standard; cDNA; 1295 BP.
cDNA encoding human PRO polypeptide #168.
US2004048333-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ65563 standard; cDNA; 1295 BP.
CODA encoding human PRO polypeptide #168.
26-FEB-2004.
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US2004058424-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ77441 standard; cDNA; 1295 BP. Human PRO polynucleotide #168. USC004038336-A1. 26-FEB-2004. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AD006098 standard; cDNA; 1295 BP.
Human PRO polynucleotide #13.
US6686451-B1.
                                                                                               CDNA; 1295 BP
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Human PRO245 gene.
WO2004031105-A2.
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Best Local Similarity , 54.0%;
                                                                                                                                                                                                                                                                                                              26-FEB-2004.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                      Query Match
Best Local Similarity
RESULT 944
                                                                                               ADM25030 standard;
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                                                                                                 Length 1295;
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                                                                                                                                                    ADII5338 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207382-A1.
                                                                                                                                                                                                                                                                                                              ADG09215 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2004009547-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA
US2003207349-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADI14670 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA
US2003207383-A1.
Leny Match (G.0%; Score 111; DB 12; Leny Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 936

ID AD15338 standard; CDNA; 1295 BP.

DE Novel human secreted and transport US-2003207382-A1.

PD D6-NOV-2007
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54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 939
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Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13.
US2003186558-A1.
CCCT-22003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI65692 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13
US2003148371-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                              6.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 942
ID ADJ99492 standard; c
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RESULT 941
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Best Local Similarity
RESULT 938
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ADT94236 standard; cDNA; 1295 BP.
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                                                                                                                                          6.0%; Score 111; DB 12; Length 1295; 54.0%; Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207354-A1.
                                                                                                                                                                                                                                                                                                   6.0%; Score 111; DB 12; 54.0%; Pred. No. 3.2e-24;
          54.0%; Pred. No. 3.2e-24;
                                                                                                                                                                                                   ADR10950 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13.
US2004137561-A1.
(GETH ) GENENTECH INC.
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US2004147017-A1.
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US2003152922-A1.
                                          ADM28285 standard; cDNA; 1295 BP. cDNA encoding human PRO polypeptide #168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AD195767 standard; cDNA; 1295 BP.
cDNA encoding human PRO polypeptide #168
US2003077659-A1.
                                                                                                                                                                                                                                                                                                                                                              ADR17859 standard; cDNA; 1295 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADT03535 standard; cDNA; 1295 BP
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54.0%;
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(GETH ) GENENTECH INC.
                                                                                                   22-APR-2004.
(GETH ) GENENTECH INC.
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WILLIAMS P.M.
WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity is
RESULT 956
ID AD195767 standard; CD
DE CDNA encoding human FF
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ASHKENAZI A.
BOTSTEIN D.
DESNOYERS L.
                                                                                                                                                        Best Local Similarity RESULT 954
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STEWART T A.
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Best Local Similarity RESULT 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FERRARA N.
FILVAROFF E
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Best Local Similarity
RESULT 959
                                                                                                                                                                                                                                                                                                                     Local Similarity
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PAONI N F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MATHER J P
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                                                                                 US2004077064-A1.
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                                                                                                                                              Query Match
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ACN40835 standard; cDNA; 1721 BP.
Tumour-associated antigenic target (TAT) cDNA DNA326887, SEQ ID NO:5879.
WO2004030615-A2.
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Human flavin-containing mono-oxygenase isoform 2 genomic sequence.
WO9824914-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACC72652 standard; cDNA; 1397 BP.
Human vascular endothelial junction-associated molecule cDNA.
WO2003025138-A2.
                                                                      Length 1295;
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Human nervous system related polynucleotide SEQ ID NO 13188.
WO200159063-A2.
                                                                    Score 111; DB 13;
Pred. No. 3.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.0%; Score 111; DB 13;
54.0%; Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.4e-24;
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Pred. No. 3.8e-24;
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(TINM) INSERM INST NAT SANTE & RECH MEDICALE.

(YMACC) 6.0%; Score 111; DB 2;

L Local Similarity 80.1%; Pred. No. 2e-23;
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80.1%; Pred. No. 1.2e-23;
                                                                                                                         ADS74498 standard; cDNA; 1295 BP.
Human secreted/transmembrane cDNA #13.
US2004185531-A1.
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                                                                    Query Match
Best Local Similarity 54.0%;
Human PRO245 cDNA sequence.
AU2003259607-A1.
27-NOV-2003.
(GETH ) GENENTECH INC.
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WILLIAMS P.M.
WOOD W I.
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PAONI N F.
ROY M A.
STEWART T A.
                                                                                                                                                                                                                                                                        FERRARA N.
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HILLAN K J
KLJAVIN I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATHER J P
                                                                                                                                                                                                                                                                                                                                                                                      GODDARD A
                                                                                                                                                                                                                                                                                                                                                                                                                        GRIMALDI
                                                                                                                                                                                                                                                                                                                                                GERBER
                                                                                                                                                                                                                                                                                                              FONG S
                                                                                                                                                                                                                                                                                                                               GAO W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (WILL/)
(WOOD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH)
                                                                                                                                                                                                                                      DESN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MATH/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PAON/
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RESULT 974
                                                                                                           ABN89533 standard; DNA; 48436 BP.
Human corneal N-acetylglucosamine-6-sulfotransferase DNA SEQ ID NO:38.
US2002061562-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADO47191 standard, DNA, 200000 BP.
DNA sequence of a human immunoglobulin heavy chain variable region.
WO2004029249-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CENT-) CENTENARY INST CANCER MEDICINE & CELL BI.
ry Match
t Local Similarity 80.1%; Pred. No. 7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2003.
(SAGR-) SAGRES DISCOVERY.
ery Match
ery Match
-- ' ... | Similarity 75.6%; Pred. No. 4.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 130207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.0%; Score 110.8; DB 12; Length 119; 98.2%; Pred. No. 8.7e-25;
                                                                                                                                                                                                                                               ADES5902 standard; DNA; 94719 BP.

Human STAT5B gene genomic DNA sequence.

WG2003039484-A2.

IS-MAY-2003.

(SAGR-) SAGRES DISCOVERY.

6.0%; Score 111; DB 10; Length 94719;

ELocal Similarity 75.6%; Pred. No. 4.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.0%; Score 111; DB 4; Length 160552; 80.1%; Pred. No. 6.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 94720;
                                                                                                                                                                                                       Length 48436;
                                                                Length 27733
Human nervous system related polynucleotide SEQ ID NO 11655.
WQ200159963-A2.
                                                                                                                                                                                                                                                                                                                                                                                          Human STATSB carcinoma associated gene, SEQ ID NO:1172 WO2003057146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD02697 standard; DNA; 160552 BP.
Human glycosyl sulfotransferase-4 (GST-4) genomic DNA.
WO200106015-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.0%; Score 111; DB 11;
Best Local Similarity 80.1%; Pred. No. 5.4e-23;
RESULT 971
                                           (HUMA-) HUMAN GENOME SCI INC.

ry Match

t Local Similarity 80.1%; Pred. No. 2.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.0%; Score 111; DB 9; 75.6%; Pred. No. 4.4e-23;
                                                                                                                                                                                                      6.0%; Score 111; DB 6;
80.1%; Pred. No. 3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACH93861 standard; DNA; 119 BP.
Human genome derived single exon probe #27056.
US2003194704-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACN44762 standard; DNA; 130207 BP. Human genomic sequence hCG21349. W02010303926-A2. (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB72392 standard, DNA; 94720 BP.
Human STAT5B gene.
WO2003008583-A2.
                                                                                                                                                                                                                                                                                                                                                                             ADA02654 standard; DNA; 94720 BP
                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2001.
(REGC ) UNIV CALIFORNIA.
Query Match
6.
                                                                                                                                  16-OCT-2003.
(PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
RESULT 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                      Best Local Similarity RESULT 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 973
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Best Local Similarity
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                              16-AUG-2001
                                                                                                                                                                                                                                                                                                                                Query Match
                                                              Query Match
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AAK87412 standard; DNA; 3504 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42224.
WO200157182-A2.
09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADQB5414 standard; cDNA; 6140 BP.
Human tumour-associated antigenic target (TAT) cDNA sequence #2228.
WO2004060270-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
(SAGR-) SAGRES DISCOVERY INC.
(SAGR-) Similarity 76.8%; Pred. No. 4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 6.0%; Score 110.8; DB 11; Length 79590; Local Similarity 79.4%; Pred. No. 4.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.0%; Score 110.8; DB 13; Length 6140; 72.5%; Pred. No. 9.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%; Score 110.8; DB 10; Length 2233; 72.5%; Pred. No. 5.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.0%; Score 110.8; DB 4; Length 3504; 77.1%; Pred. No. 6.9e-24;
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                                                                                                                                     Length 128;
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Human hCG77579 carcinoma associated gene, SEQ ID NO:1592.
WO2003057146-A2.
                                                                                                                                                                               мынызывич standard; cDNA; 567 BP.
Human colon cancer antigen encoding cDNA SEQ ID NO:860.
WO200122920-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADQ97343 standard; DNA; 61739 BP.
Human cancer associated sequence HD08-035, SEQ ID 320.
WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK69827 standard; DNA; 4002 BP.
Human secreted protein gene 14 genomic DNA fragment
WO200226931-A2.
                                                                                                                                                                                                                                                                       PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 76.8%; Pred. No. 2.3e-24;
RESULT 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HJWA-) HUMAN GENOME SCI INC.

(HJWA-) HUMAN GENOME SCI INC.

6.0%; Score 110.8; DB 6;

(ery Match inity 72.5%; Pred. No. 7.5e-24;
                                                                                                                                   6.0%; Score 110.8; DB 5; 98.2%; Pred. No. 9.1e-25;
AAF65710 standard; cDNA; 128 BP.
Novel human polynucleotide, SEQ ID NO: 1466.
WQ200102568-A2.
I-JAN-2001.
(CHIR.) CHIRON CORP.
(HYSE.) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADL27152 standard; DNA; 79590 BP.
Human genomic sequence for hCG27579 #2.
US2003216588-A1.
20-NOV2-003.
(MORR) MORRIS D W.
(ENGE/) ENGELHARD E K.
                                                                                                                                                                                                                                                                                                                                                                               ADA53157 standard; cDNA; 2233 BP. Human coding sequence, SEQ ID 725 EP1293569-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUL-2004.
(GETH ) GENENTECH INC.
(WUTD/) WU T D.
(ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 977
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Best Local Similarity
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RESULT 980
                                                                                                                                                 Best Local Similarity
RESULT 975
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABO99278 standard; cDNA; 1472 BP. Human coding sequence SEQ ID 11. W0200259250-A2. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX80486 standard; cDNA; 2791 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 78.7%;
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(GENY ) GENETICS INST INC.
(CEY Match 6.0%;
                                   6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.0%;
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PA (GEMY ) GENETICS INST INC.

QUEYY MATCh

6.0%;

BEST Local Similarity 78.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCCOY J M.
LAVALLIE E R.
COLLINS-RAÇIE L A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TREACY M.
AGOSTINO M J.
STEININGER R J.
                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NEWO-) NEWORGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-2004.
(NUVE-) NUVELO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVANS C. MERBERG D.
                                                    Best Local Similarity RESULT 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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RESULT 997
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Best Local Similarity
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JACO/) JACOBS K.
                                                                                                                                                                                                                                                                                                                                                                                                                               19-FEB-2004
                                                                                                                                                                                                       15-APR-200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MCCO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EVAN/)
(MERB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 6.0%; Score 110.8; DB 13; Length 117750;

BBSE Local Similarity 80.2%; Pred. No. 5.9e-23;

RESULT 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vuery Match 6.0%; Score 110.8; DB 10; Length 79684;
Best Local Similarity 79.4%; Pred. No. 4.6e-23;
RESULT 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12; Length 119501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 270150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%; Score 110.8; DB 11; Length 94330; 81.1%; Pred. No. 5.1e-23;
                                                             Score 110.8; DB 9; Length 79684;
Pred. No. 4.6e-23;
                                                                                                                                                                                                                                                                             Query Match 6.0%; Score 110.8; DB 9; Length 79684; Best Local Similarity 79.4%; Pred. No. 4.6e-23; RESULT 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
ry Match
t Local Similarity 79.8%; Pred. No. 2.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             App65796 standard; DNA; 270150 BP.

Human 16p133 sequence section 7 of 8 DNA.
W02003072827-A1.
04-SEP-2003.
(CHL-) CHILDREN'S HOSPITAL MEDICAL CENT.
6.0%; Score 110.8; DB 11
ELOCAL Similarity 72.5%; Pred. No. 9.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.0%; Score 110.8; DB 1.83.0%; Pred. No. 5.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.0%; Score 110.6; DB 5 79.8%; Pred. No. 2.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABD32653 standard; DNA; 117750 BP.
Human cancer-associated genomic DNA HD13-060.
WO2004074320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL37082 standard; DNA; 526 BP.
Human ovarian cancer DNA marker #10972.
WO200170979-A2.
27-SEP-2001.
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                      ADA66358 standard; DNA; 79684 BP.
Human hCG27579 gene genomic DNA sequence.
MO3-JUL-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADL43466 standard; DNA; 584 BP.
Human ovarian cancer DNA marker #17356.
W0200170979-A2.
27-SEP-2001.
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Human ovarian cancer DNA marker #4673.
WO200170979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADI29095 standard; DNA; 119501 BP.
Human MARK3 genomic DNA.
US2003232771-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACN44662 standard; DNA; 94330 BP. Human genomic sequence hCG20930. W020030073826-A2. 12-SEP-2003. (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                        ADB72812 standard; DNA; 79684 BP
PD 17-JUL-2003.

PA (SAGR-) SAGRES DISCOVERY.

QUETY MATCh

Best Local Similarity 79.4%;

RESULT 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2003.
(ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human hCG27579 gene.
WO2003008583-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
RESULT 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BEREE
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ACN39479 standard; cDNA; 1341 BP.
Tumour-associated antigenic target (TAT) cDNA DNA325690, SEQ ID NO:3643.
WO2004030615-A2.
                                                                                                                                                                                                         Match 6.0%; Score 110.6; DB 13; Length 1341; Local Similarity 78.7%; Pred. No. 4.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 110.6; DB 10; Length 1697; Pred. No. 5.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.0%; Score 110.6; DB 13; Length 1697; 78.7%; Pred. No. 5.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.0%; Score 110.6; DB 6; Length 1472; 78.7%; Pred. No. 4.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 110.6; DB 2; Length 2791; Pred. No. 6.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 110.6; DB 4; Length 2791; Pred. No. 6.9e-24;
Score 110.6; DB 5; Length 584;
Pred. No. 2.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 110.6; DB 12;
Pred. No. 4.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel DNA-related contig nucleotide sequence #19 W02003054122-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS59232 standard; cDNA; 2791 BP.
Human cDNA encoding a secreted protein yc2_1.
WO200175068-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADS11156 standard; DNA; 1697 BP.
Human therapeutic contig DNA - SEQ ID 1393.
WO2004080148-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein yc2_1 encoding cDNA.W09932614-A1.
                                                                                                                                                                                                                                                                                     ADK00610 standard; DNA; 1388 BP.
HOMO protein encoding sequence #11.
WO2004014946-Al.
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Score 110.6; DB 11; Length 110000;
Pred. No. 6.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 110000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
6.0%; Score 110.6; DB 3; Length 138169;
Best Local Similarity 80.4%; Pred. No. 7.5e-23;
RESULT 1008
ID ABD20695 standard; DNA; 141586 BP.
DE Human pulmonary and inflammatory target DNA #306.
PN WOO205309-A2.
PN (EPIG-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.0%; Score 110.6; DB 11; Length 141586; 80.4%; Pred. No. 7.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AD055274 standard; DNA; 99100 BP.
Human cyclin-dependent kinase 10, CDK10, genomic sequence.
Query Match
6.0%; Score 110.6; DB 12; Length 99100;
BBSt Local Similarity 80.4%; Pred. No. 6.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 79544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 110.6; DB 3; Length 141589;
Pred. No. 7.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 50000;
                                                                                                                                                                                                                                                                                                                                     16-40G-2001.
(HUMA-) HUMAN GENOME SCI INC.
(ery Match
ery Match
(ery Match 80.4%; Pred. No. 1.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA34791 standard; DNA; 138169 BP.
Human adenosine receptor related polynucleotide SEQ ID NO:2480.
W0200009525-A2.
24-FEB-2000.
(UYEC-) UNIV EAST CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA35005 standard; DNA; 141589 BP.
Human adenosine receptor related polynucleotide SEQ ID NO:2694
WO200009525-A2.
                                                                          6.0%; Score 110.6; DB 6; Length 2791; 78.7%; Pred. No. 6.9e-24;
                                                                                                                                                                                                                              4; Length 3775;
                                                                                                                                                                                                                                                                                 ABA20373 standard; DNA; 12328 BP.
Human nervous system related polynucleotide SEQ ID NO 12704.
WO200159063-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ97764 standard; DNA; 79544 BP.
Human cancer associated sequence HD10-042, SEQ ID 741.
WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S2-UUL-2004.
(SACR-) SAGRES DISCOVERY INC.
(SACR-) AGRES DISCOVERY INC.
6.0%; Score 110.6; DB 12;
ery Match
78.7%; Pred. No. 5.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 110.6; DB 11;
Pred. No. 6.6e-23;
                                                                                                                                                                                                                              6.0%; Score 110.6; DB 4 70.0%; Pred. No. 8.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.0%; Score 110.6; DB 1
75.8%; Pred. No. 4.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                AAIG1061 standard; cDNA; 3775 BP.
Human polynucleotide SEQ ID NO 5050.
WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC60735 standard; DNA; 50000 BP.
Human alingshot-related DNA 9.
JP2003102483-A.
08-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2002,
(EPIG-) EPIGENESIS PHARM INC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.0%;
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Q (UYEC-) UNIV EAST CAROLINA.

Q (UYEC-) MICH

Best Local Similarity 80.4%;
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2002.
1G-) EPIGENESIS F.
ETY MATCh
Best Local Similarity 81
RESULT 1009
ID AAA35005 standar
DE Human adence
PN WO20000
A (SPAU/) SPAULDING V.
A (WONG/) WONG G G.
A (CLARK) CLARK H.
A (FECH/) FECHTEL K.
Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
RESULT 1004
ID ADO56274 standard; DE Human cyclin-dependi
                                                                                                                                                                                                                                            Best Local Similarity RESULT 1001
                                                                                          Best Local Similarity RESULT 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
RESULT 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
RESULT 1007
                                                                                                                                                                                         26-JUL-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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mu200265109-A2.

PD 31-OCT-2002.

PA (EPIG-2002.)

PA (EPIG-2002.)

PA (EPIG-2002.)

PA (EPIG-2002.)

PA (EPIG-2002.)

PA (EPIG-2002.)

Bast Local Similarity 80.4%; Pred. No. 7.7e-23; RESULT 1018

ID ABD19162 standard; DNA; 141601 BP.

PB (WO200285309-A2.)

PA (FIGH-1 DNA fragment #2.)

PA (FIGH-1 DNA fragment #2.)

PA (FIGH-1 DNA fragment #2.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mu200285308-A2.

PD 31-OCT-2002.

PA (EPIG-) EPIGENESIS PHARM INC.

Query Match

Bast Local Similarity 80.4%; Pred. No. 7.7e-23;

ID ABZ96607 standard; DNA; 141589 BP.

Br woon 5.4%; Pred. No. 7.7e-23;

PA WOO02085308-A2.

PD 31-OCT-2002

PA (FPIG-) PA (FPIGENESIS PHARM INC.

ACCOUNTY MACCH SIMILARITY 80.4%; Pred. No. 7.7e-23;

PA (FPIG-) PA (FPIGENESIS PHARM INC.

Br WOOD0285308-A2.

PA (FPIG-) PA (FPIGENESIS PHARM INC.

PA (FPIGENESIS PHARM INC.)

PA (FPIGENESIS PHARM INC.)

PA (FPIGENESIS PHARM INC.)

PA (FPIGENESIS PHARM INC.)
                                                                                                                                                                                                                         AAF21152 standard; DNA; 141589 BP.
Human low adenosine antisense oligonucleotide related sequence #2719.
WO200062736-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF21127 standard; DNA; 141589 BP.
Human low adenosine antisense oligonucleotide related sequence #2694.
WO200062736-A2.
26-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 110.6; DB 10; Length 141589; Best Local Similarity 80.4%; Pred. No. 7.7e-23; RESULT 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-2002.
(EPIG-) EPIGENESIS PHARM INC.
(ery Match 6.0%; Score 110.6; DB 10; Length 141589;
                                                                                                                                                                                                                                                                                                                                                                                6.0%; Score 110.6; DB 3; Length 141589; 80.4%; Pred. No. 7.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.0%; Score 110.6; DB 3; Length 141589; 80.4%; Pred. No. 7.7e-23;
ID AAA35030 standard, DNA; 141589 BP.

ID AAA35030 standard, DNA; 141589 BP.

PH Human adenosine receptor related polynucleotide SEQ ID NO:2719.

PN WO200009525-A2.

PD 24-FEB-2000.

PA (UYEC-) UNIV EAST CAROLINA.

Query Match (6.0%; Score 110.6; DB 3; Length 141589 Best Local Similarity 80.4%; Pred. No. 7.7e-23;

RESULT 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                     JT 1012
AAF20913 standard; DNA; 141589 BP.
Human ELAM-1 polynucleotide fragment #2480.
WO200062736-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABZ96846 standard; DNA; 141589 BP.
Human nucleic acid sequence.
WO200285308-A2.
                                                                                                                                                                                                                                                                                                                                  (UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYEC-) UNIV EAST CAROLINA (NYCE/) NYCE J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
RESULT 1013
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1012
                                                                                                                                                                                                                                                                                                          26-OCT-2000
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PD 31-0CT-2002.

PD 31-0CT-2002.

PA (EPIG-) EPIGENESIS PHARM INC.

Query Match

BEST Local Similarity 80.4%; Pred. No. 9.7e-23;

RESULT 1024

ID ABD17970 standard; DNA; 209284 BP.

DE Human factor-related antisense pol---

PD 31-0CT-2002.

PA (FIG. 10.6) DB 10; Length 209274;

PD ABD17970 standard; DNA; 209284 BP.

DE Human factor-related antisense pol---

PD 31-0CT-2002.

PA (FIG. 10.6) DB 10; Length 209274;

PD ABD17970 standard; DNA; 209284 BP.

PD A (FIG. 10.6) DB 10; Length 209274;

PD A (FIG. 10.6) DB 10; Length 209274;
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Human musculoskeletal system related polynucleotide SEQ ID NO 788.
WO200155367-Al.
02-AUG-2001.
     6.0%; Score 110.6; DB 11; Length 141601; 80.4%; Pred. No. 7.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11; Length 146984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENESIS PHARM INC.
ry Match
6.0%; Score 110.6; DB 11; Length 209284;
L Local Similarity 80.4%; Pred. No. 9.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.0%; Score 110.6; DB 11; Length 248436; 77.2%; Pred. No. 1.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 146982;
                                                                                                                                                                                                                                   6.0%; Score 110.6; DB 3; Length 146981; 80.4%; Pred. No. 7.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
(SAGR-) SAGRES DISCOVERY.
6ry Match
6ry Match
68.5%; Pred. No. 2.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF21437 standard; DNA; 209273 BP.
Human factor-related antisense polynucleotide #3004.
WO200062736-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                              cuery Match 6.0%; Score 110.6; DB 10
Best Local Similarity 80.4%; Pred. No. 7.8e-23;
RESULT 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.0%; Score 110.6; DB 1:
Best Local Similarity 80.4%; Pred. No. 7.8e-23;
                                                                             AAF21442 standard; DNA; 146981 BP.
Human ELAM-1 polynucleotide fragment #3009.
WO200062736-A2.
                                                                                                                                                                                                                                                        Best Local Similarity 80.4%; Pred. No. 7 RESULT 1020
ID ABZ97136 standard; DNA; 146982 BP.
DE Human ELAM-1 antisense fragment no.1738. PN WO200253508-A2.
PN WO200255308-A2.
PN (EPIG-2002.)
PA (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABD19160 standard; DNA; 146984 BP.
Human BLAM-1 DNA fragment 1738.
WO200285309-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACN45190 standard; DNA; 248436 BP.
Human genomic sequence hCG16330.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACN44670 standard; DNA; 22021 BP.
Human genomic sequence hCG20786.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-2002.
(EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                   26-OCT-2000.
(UYEC-) UNIV EAST CAROLINA.
(NYCE/) NYCE J W. 6 0%:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-OCT-2000.
(UYEC-) UNIV EAST CAROLINA.
(NYCE/) NYCE J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1027
Query Match
Best Local Similarity
RESULT 1019
ID AAF21442 standard: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
RESULT 1025
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1022
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ADJ12650 standard; DNA; 16422 BP.
DNA fragment of a BAC clone that encodes a human secreted protein Seg504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vuery match 6.0%; Score 110.2; DB 12; Length 16422;
Best Local Similarity 80.7%; Pred. No. 2.8e-23;
RESULT 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-2003.
\( (SAGR-) SAGRES DISCOVERY.
Query Match
6.0%; Score 110.2; DB 11; Length 39148;
Best Local Similarity 80.7%; Pred. No. 4.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 21581;
                                                                                                                                                                                                                                                                                           ADJ28161 standard, DNA, 612 BP.
Human musculoskeletal system-associated contig DNA - SEQ ID 788.
US2004009488-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAY-2004.
(GETH ) GENENTECH INC.
ery Match 6.0%; Score 110.2; DB 12; Length 6905;
gt Local Similarity 80.7%; Pred. No. 1.6e-23;
                                                                                                                                                                                                                                                                                                                                                     Length 6905;
                                 Dest Local Similarity 80.7%; Pred. No. 3.7e-24;
RESULT 1028
ID ABX58434 standard; cDNA; 612 BP.
DE CDNA encoding novel human musculoskeletal system antigen #778.
PN US2002147140-A1.
               6.0%; Score 110.2; DB 4; Length 612; 80.7%; Pred. No. 3.7e-24;
                                                                                                                                                                                                                                      Length 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID ADC87234 standard; DNA; 21581 BP.
DE Human GPCR gene SEQ ID NO:1687.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY.
QUETY MATCH
Beet Local Similarity 74.7%; Pred. No. 3.3e-23;
PRESULT 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD 29-JUN-1995.

PA (IMMU-) IMMUNOBIOLOGY RES INST INC.

Query Match 6.0%; Score 110.2; DB 2;

Best Local Similarity 80.7%; Pred. No. 1.6e-23;

RESULT 1031
                                                                                                                                                                                                                                  6.0%; Score 110.2; DB 8; 80.7%; Pred. No. 3.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ92779 standard; DNA; 6905 BP.
Human thymopoietin continuous gene fragment.
WO9517205-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 1034
ACN43878 standard, DNA, 39148 BP.
Human genomic sequence hCG36720.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AD019382 standard; DNA; 6905 BP.
Human PRO polynucleotide #720.
WO2004043361-A2.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RUBEN S M.
FLORENCE K A.
GREENE J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FLOR)) FLORENCE K A (GREE) GREENE J M. (YOUN) YOUNG P E. (YOUN) YOUNG P E. (YUGG) YU G. (FLOR)) FLORENCE C. (EBNE) EBNER H. (OLSE)) OLSEN H.
                                                                                                                                                               (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                               Best Local Similarity
RESULT 1029
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BREWER L A.
DUAN R D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2004010132-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JAN-2004,
(ROSE/) ROSF
                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BREW/) I
(DUAN/) I
(RUBE/)
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(PATH-) PATHOARRAY GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1047
                      Query Match
Best Local Similarity
RESULT 1044
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RESULT 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Si
RESULT 1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL36242 standard; DNA; 5199 BP.
Human musculoskeletal system related polynucleotide SEQ ID NO 2607.
WO200155367-A1.
                                                                                                                                                                          AAL16240 standard; DNA; 5157 BP.
Human musculoskeletal system related polynucleotide SEQ ID NO 2605.
WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human musculoskeletal system-associated genomic DNA - SEQ ID 2605.
US2004009488-A1.
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US2004009488-A1.
RESULT 1035

ID ABD33115 standard; DNA; 69652 BP.

DE Human cancer-associated (CA) gene HD07-011.

PN WO2004058146-A2.

PD 15-JUJ-2004.

PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 6.0%; Score 110.2; DB 13; Length 69652;

RESULT 1036

RESULT 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABX59230 standard; cDNA, 5199 BP.
CDNA encoding novel human musculoskeletal system antigen #1574.
US2002147140-A1.
10-OCT-2002.
(ROSE), ROSEN C A.
(RUSE), RUSEN S M.
(BARA), BARASH S C.
                                                                                                                                                                                                                                                                                                                                  ABXS5228 standard; cDNA; 5157 BP.
cDNA encoding novel human musculoskeletal system antigen #1572.
US2002147140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JAN-2004.
(HUMA-) HUMAN GENOME SCI INC.
(ery Match
ery Match
(ery Match 1:6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 16707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.

6.0%; Score 110; DB 12; Length 5157;

it Local Similarity 80.0%; Pred. No. 1.6e-23;
                                                                                                                                                                                                                                                                               Length 5157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 5157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 5199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 5199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-AUG-2011.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
6-17 Match
(ery Match 60.0%; Score 110; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.0%; Score 110; DB 8;
80.0%; Pred. No. 1.6e-23;
                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.

ry Match
6.0%; Score 110; DB 4;
t Local Similarity 80.0%; Pred. No. 1.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.0%; Score 110; DB 2; 76.9%; Pred. No. 3.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.0%; Score 110; DB 8;
80.0%; Pred. No. 1.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACA64895 standard; DNA; 134292 BP.
Human GABBR1 DNA corresponding to AL031983.
DE10127572-A1.
05-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX58061 standard; DNA; 16707 BP.
Genomic DNA for Human GABAB receptors
WO9921890-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ29980 standard; DNA; 5199 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ29978 standard; DNA; 5157 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jobe

JSG-A1.

Jode-) HUMAN GENON.

JCY MAtch

Jest Local Similarity 6

JCSULT 1040

ID ABX59230 standar<sup>2</sup>

DE CDNA encoding

PN US20021471<sup>2</sup>

PN US20021471<sup>2</sup>

PA (ROSP

PA (P)
                                                                                                                                                                                                                                                                                                                                                                                                       ABRASH S C.
AZA/) BARASH S C.
AZY MATCh
Beet Local Similarity PRESULT 1038
ID ADJ29978 stand**
DE Human musc**
PN US2004**
PD 15**
PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 1039
ID AAL36242 standard; DN
DE Human musculoskeletal
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME 8
                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2002.
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 1042
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Best Local Similarity
RESULT 1041
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(ASTR ) ASTRA AB.
                                                                                                                                                                                                                                       02-AUG-2001
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1D ABX59220
DE CDNA enc
PN US20021-
PD 10-OCT--
PA (ROBE/)
PA (RUBE/)
PA (RABE/)
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Best Local Similarity 69.3%; Pred. No. 3.16-23;
RESULT 1046
ID AAK89916 standard; DNA; 12288 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3492.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME CTT TYC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK89917 standard; DNA; 14495 BP.
Human digestive system antigen genomic sequence SEQ ID NO: 3493.
WO200155314-A2.
(2-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK89915 standard; DNA; 14484 BP.
Human digestive system antigen genomic sequence SEQ ID NO: 3491
WO200155314-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LUCLY MATCH 6.0%; Score 109.8; DB 4; Length 14495; Best Local Similarity 69.3%; Pred. No. 3.4e-23; RESULT 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) 02-AUG-2001.
A (HUMA-) HUMAN GENOME SCI INC.
Query Match , 6.0%; Score 109.8; DB 4; Length 32193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.0%; Score 109.8; DB 4; Length 12288; 69.3%; Pred. No. 3.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 14484;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 32193;
  Length 134292;
                                                                                                                                           PD 25-WAR-1999.

PA (GETH ) GENENTECH INC.

Query Natch
6.0%; Score 109.8; DB 2; Length 114;
Best Local Similarity 97.4%; Pred. No. 1.8e-24;
RESULT 1045
ID ABA07271 standard; DNA; 12288 BP.
                                                                                                                                                                                                                                                              ABA07271 standard; DNA; 12288 BP.
Human pancreatic cancer related genomic DNA, SEQ ID NO:
W0200155206-A1.
02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
ery Match
foot Similarity 69.3%; Pred. No. 3.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABA07270 standard; DNA; 14484 BP.
Human pancreatic cancer related genomic DNA, SEQ ID NO:
WO200155206-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PA (HUVA-) HUVAN GENOME SCI INC.

Query Match
Best Local Similarity 69.3%; Pred. No. 3.4e-23;
RESULT 1049
ID ABA07272 standard; DNA; 14495 BP.

DE Human pancreatic cancer related genomic DNA, SEQ ID
PN WO200155206-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human novel protein-encoding gene 7, SEQ ID NO:37, 02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
focal Similarity '69.3%; Pred. No. 3.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 109.8; DB 4;
Pred. No. 5.6e-23;
6.0%; Score 110; DB 8; 76.9%; Pred. No. 1.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD16595 standard; DNA; 32193 BP
                                                                   AAX56603 standard; DNA; 114 BP.
Human 345566 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
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(HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                       Query Match
                         Query Match
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Best Local Similarity 79.3%; Pred. No. 9.8e-23; RESULT 1058

ID ADA66358 standard; DNA; 79684 BP.

BE Human hCG27579 gene genomic DNA ...

PN WC2003053224-A2.

PA (2010)
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WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                Human musculoskeletal system-associated genomic DNA - SEQ ID 2623
US2004009488-A1.
                                                                                                                                                                                                                                                                                                                                                                         15-JAN-2004.
(HUMA-) HUMAN GENOME SCI INC.
(HVMA-) HUMAN GENOME SCI INC.
ery Match
ery Match
79.6%; Pred. No. 5.6e-23;
                                                                                                                                                                                                                                                                                  6.0%; Score 109.8; DB 10; Length 32193; 79.6%; Pred. No. 5.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 79590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 79684;
                                 ABX59246 standard; cDNA; 32193 BP.
cDNA encoding novel human musculoskeletal system antigen #1590.
US2002147140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1516;
                                                                                                                                                   Length 32193,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9; Length 79684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADL09133 standard; CDNA; 1516 BP.
Human protein phosphatase 2A alpha subunit 22. 66,
CN1355310-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%; Score 109.6; DB 10; 78.4%; Pred. No. 1e-23;
                                                                                                                                                   6.0%; Score 109.8; DB 8; 79.6%; Pred. No. 5.6e-23;
                                                                                                                                                                                                                Genomic DNA encoding human NOVX protein seq id 37 US2003207285-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 109.8; DB 9
Pred. No. 9.8e-23;
      79.6%; Pred. No. 5.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.0%; Score 109.8; DB 1
Best Local Similarity 79.3%; Pred. No. 9.7e-23;
RESULT 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.0%; Score 109.8; DB 1 79.3%; Pred. No. 9.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADL27152 standard; DNA; 79590 BP.
Human genomic sequence for hCG27579 #2.
US2003216558-Al.
                                                                                                                                                                                                   ADG62943 standard; DNA; 32193 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB72812 standard; DNA; 79684 BP.
Human hCG27579 gene.
WC2003008583-A2.
                                                                                                                                                                                                                                                                                                                                  DNA; 32193 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL36348 standard; DNA; 19820 BP
                                                                                                                                                                                                                                              06-NOV-2003.
(HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MORR/) MORRIS D W. (ENGE/) ENGELHARD B K.
                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1055
                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 1060
                                                                                                   (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-2002.
(UYFU-) UNIV FUDAN.
Best Local Similarity
RESULT 1053
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
RESULT 1061
                                                                                                                                                                                                                                                                                                                                 ADJ29996 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-200
                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                   RESULT 1054
                                      BABBBBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A D S E D
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Human musculoskeletal system-associated genomic DNA - SEQ ID 2713
US2004009488-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                    15-JAN-2004.
(HUMA-) HUMAN GENOME SCI INC.
lery Match
lery Match
5-7-1 Similarity 74.5%; Pred. No. 4.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 37904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK87217 standard; DNA; 30709 BP.

3 Human lipase, hormone-sensitive (LIPE) gene sequence.

Query Match
6.0%; Score 109.6; DB 6; Length 30709;

Best Local Similarity 78.6%; Pred. No. 6.3e-23;
  4; Length 19820;
                                                                         ABX59336 standard; cDNA; 19820 BP.
cDNA encoding novel human musculoskeletal system antigen #1680.
US2002147140-Al.
                                                                                                                                                                                                                                                          8; Length 19820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD 07-FEB-2001.

Query Match. HELLY RES INST.

Query Match
Best Local Similarity 79.6%; Pred. No. 6.4e-24;

RESULT 1069

ID AAHIBIS60 standard; CDNA, 949 BP.

DE Human CDNA sequence SEQ ID NO:18397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PA (HELL-) HELIX RES INST.

Query Match

Best Local Similarity 79.6%; Pred. No. 8.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

Query Match 6.0%; Score 109.6; DB 10;

Best Local Similarity 77.1%; Pred. No. 7.2e-23;

RESULT 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.9%; Score 109.4; DB 5;
Best Local Similarity 98.4%; Pred. No. 6.3e-24;
RESULT 1068
                                                                                                                                                                                                                                                     6.0%; Score 109.6; DB 8.74.5%; Pred. No. 4.8e-23;
6.0%; Score 109.6; DB 4 74.5%; Pred. No. 4.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH09279 standard, cDNA, 573 BP.
Human cDNA clone (3'-primer) SEQ ID NO:6114.
EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABV00481 standard; cDNA; 550 BP.
Human prostate expression marker cDNA 3472.
WO200160860-A2.
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Human endozepine-like protein NOV1c cDNA.
US2003195149-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACN44966 standard; DNA; 125534 BP.
Human genomic sequence hCG32986.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC87244 standard; DNA; 37904 BP. Human GPCR gene SEQ ID NO:1697. EP1270724-A2.
                                                                                                                                                                                                                                                                                                                               ADJ30086 standard; DNA; 19820 BP.
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(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                   10-OCT-2002.
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GANG/) GANGOLLI E A.
                     Best Local Similarity
RESULT 1062
                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
RESULT 1064
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Best Local Similarity
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PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
PA (PROT-) PROTEIN EXPRESS KK.
Query Match 5.9%; Score 109.4; DB 10; Length 3682;
Best Local Similarity 71.5%; Pred. No. 2e-23;
RESULT 1073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 71.5%; Pred. No. 2.1e-23;
RESULT 1075
Best Local Similarity 71.5%; Pred. No. 2.1e-23;
RESULT 1075
Best Local Similarity 71.5%; Pred. No. 2.1e-23;
Best Local Similarity 71.5%; Pred. No. 2.1e-23; Pred. No. 2.1e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.9%; Score 109.4; DB 6; Length 3887; 71.5%; Pred. No. 2.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.9%; Score 109.4; DB 6; Length 3920; 71.5%; Pred. No. 2.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Length 3920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK90191 standard; DNA; 28506 BP.
Human flavin containing monooxygenase-2 (FMO2) gene sequence.
WO200253579-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD72116 standard; cDNA; 3920 BP.

Human endozepine-like protein NOV1a cDNA NOV1b.
US2003195149-A1.
16-OCT-2003.
(GANG) GANGOLLI E A.
(STON/) STONE D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 109.4; DB 6
Pred. No. 2.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAL43754 standard; DNA; 3887 BP. Human NOV1a gene sequence. Woo200244211-A2. 06-JUN-2002. (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAL43756 standard; DNA; 3920 BP.
Human NOVIC gene sequence.
WO200244211-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.9%;
Best Local Similarity 71.5%;
RESULT 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human NOV1b gene sequence. WO200244211-A2. 06-JUN-2002. (CURA-) CURAGEN CORP.
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2002.
2002.
2AA-) CURAGEN CORP
2-rY Match
Best Local Similarity 77
RESULT 1076
ID AAL43755 standa-
DE Human NOV1P
PN WO20024.
PD 06-
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(CURA-) CURAGEN CORP.
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(CURA-) CURAGEN CORP.
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RESULT 1079
ID ABK90191 standard, DN.
DE Human flavin containin
PN W0200253579-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
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Best Local Similarity
RESULT 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-2002
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AAD11633 standard; cDNA; 1458 BP.
Human secreted protein-encoding gene 4 cDNA clone HAMGG68, SEQ ID NO:14.
WO200151504-A1.
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PA (SAGR-) SAGRES DISCOVERY INC.

Query Match

Guery Match

5.9%; Score 109.4; DB 12; Length 257645;

Best Local Similarity 79.6%; Pred. No. 2.7e-22;

RESULT 1083

The AAK76583 standard; DNA; 984 BP.

DB Human immune/Daematopoietic antigen genomic sequence SEQ ID NO:31395.

PN W0200157182-A2.
                                                                                                                                                                                                     ADBIG527 standard; DNA; 49806 BP.
Human DYXC1 DNA, chromosomal gene region nucleotides 50001-100000
WO2003068814-A1.
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ID AA238020 standard; cDNA; 1458 BP.
DB Human secreted protein encoding nucleotide sequence SEQ ID NO:14
PN WO200004140-A1.
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                                                                       Length 28506;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 49806;
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(HUMA-) HUMAN GENOME SCI INC.
S.9%; Score 109.2; DB 6; Length 1458;
T.1%; Pred. No. 1.3e-23;
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ry Match
5.9%; Score 109.2; DB 4; Length 1458;
t Local Similarity 72.1%; Pred. No. 1.3e-23;
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                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 79.6%; Score 109.4; DB 9; RESULT 10cal Similarity 79.6%; Pred. No. 9.8e-23; ID ADR53001 standard; DNA; 96256 BP.

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Human cancer associated sequence HD08-026, SEQ ID
WO2004060304-A2.
                                                                       Query Match 5.9%; Score 109.4; DB 6; Best Local Similarity 79.6%; Pred. No. 7e-23; RESULT 1080
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(HUWA-) HUMAN GENOME SCI INC.
5.9%; Score 109.2; DB 3;
ery Match
cery match
72.1%; Pred. No. 1.3e-23;
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A (HUWA-) HUWAN GENOME SCI INC.
Query Match 5.9%; Score 109.2; DB 4;
Best Local Similarity 78.9%; Pred. No. 1e-23;
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Human secreted protein encoding cDNA.
W02002102993.A2.
27-DEC-2002.
(HUMA-) HUMAN GENOME SCI INC.
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11-JUL-2002.
(GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein gene 4. WO200226931-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BURC/) BURCZYNSKI M.
(TWIN/) TWINE N.
(DORN/) DORNER A J.
(TREP/) TREPICCHIO W L.
                                                                                                                                                                                                                                                                                                                                        21-AUG-2003.
(LICN ) LICENTIA LTD.
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Human secreted protein-related DNA sequence - SEQ ID No 259
                                                                                              03-OCT-2002.
(HUMA-) HUMAN GENOME SCI INC.
                                                         WO200277188-A2.
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ID ABT16905 cornal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) 16-AUG-2001.

(HUMA-) HUMAN GENOME SCI INC.

Query Match 5.9%; Score 109.2; DB 5; Length 32134;

Best Local Similarity 82.4%; Pred. No. 8.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.9%; Score 109.2; DB 4; Length 31931; 78.9%; Pred. No. 8.7e-23;
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                                                                                                                                                                                                                                                          Length 1458;
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Human reproductive system related antigen DNA SEQ ID NO: 6763
WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA07160 standard; DNA; 31931 BP.
Human pancreatic cancer related genomic DNA, SEQ ID NO: 479.
WO200155206-Al.
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PW W020015905-A2.

PD 16-AUG-2001.

PA (HUMA-) HTMAN A COMPANDA STATES A C
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Human nervous system related polynucleotide SEQ ID NO 7685.
WO200159063-A2.
                                                                                                        PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 72.1%; Pred. No. 1.3e-23;
RESULT 1089
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                                    Human secreted protein coding sequence, SEQ ID 26 WO200295010-A2.
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Human secreted protein-related DNA sequence #84.
WO200292787-A2.
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                                                                                                                                                                                                                                                                                                                                                                                             ADE72775 standard; DNA; 1784 BP.
Human endometrial specific gene, SEQ ID NO 215.
WO2003060081-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE72772 standard; DNA; 3199 BP.
Human endometrial specific gene, SEQ ID NO 212.
WO2003060081-A2.
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Ouery Match
ACC50359 Btandard; cDNA; 1458 BP.
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(DIAD-) DIADEXUS INC.
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(DIAD-) DIADEXUS INC.
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RESULT 1092
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Best Local Similarity
RESULT 1093
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RESULT 1094
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Score 109.2; DB 11; Length 128668; Pred. No. 2e-22;
                                                                                                                                                                                               Length 51961;
                  Length 51961
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Human digestive system antigen genomic sequence SEQ ID NO: 4741
WO200155314-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL99497 standard; DNA; 15514 BP.
Human testicular antigen encoding DNA fragment SEQ ID NO: 3149.
WO200155317-A2.
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Human testicular antigen encoding DNA fragment SEQ ID NO: 3150.
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ry Match
t Local Similarity 79.9%; Pred. No. 5.4e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABA07434 standard; DNA; 11532 BP.
Human pancreatic cancer related genomic DNA, SEQ ID NO: 753.
WO200155206-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 11532;
                                                                             ABZ67488 standard, DNA, 51961 BP.
Human secreted protein encoding genomic DNA SEQ ID NO 1011.
03-0027-186-A2.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AALOS933 standard; DNA; 15514 BP.
Human reproductive system related antigen DNA SEQ ID NO:
WO200155320-A2.
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Query Match
5.9%; Score 109; DB 4; Lengt
Best Local Similarity 76.7%; Pred. No. 6.5e-23;
RESULT 1105
ID ALGOS94 standard; DNA; 15517 BP.
DE Human reproductive system related antigen DNA SEQ ID.
PN, WO200155320-A2.
                                                                                                                                                                                           Query Match 5.9%; Score 109.2; DB 10; Best Local Similarity 78.9%; Pred. No. 1.2e-22;
Query Match 5.9%; Score 109.2; DB 10; Beet Local Similarity 78.9%; Pred. No. 1.2e-22; RESULT 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.9%; Score 109; DB 13; 78.3%; Pred. No. 1.7e-23;
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(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.9%; Score 109; DB 4;
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Match
Local Similarity 76.7%; Pred. No. 6.5e-23;
                                                                                                                                                                                                                                            Luman genomic sequence hCG40471. WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADS09792 standard; DNA; 1785 BP.
Human therapeutic DNA - SEQ ID 29.
WO2004080148-A2.
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                                                                                                                                                                                                                                                                                                                             12-SEP-2003.
A (SAGR.) SAGRES DISCOVERY.
A (PACH.) Best Local Similarity 78.9%;
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(NUVE-) NUVELO INC.
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RESULT 1103
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RESULT 1104
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Best Local Similarity
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Best Local
RESULT 1119
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30980.
WO200157182-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS28363 standard; DNA; 32146 BP.
Genomic sequence #203 encoding for novel human respiratory antigen.
WO200155448-A1.
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Genomic sequence #208 encoding for novel human respiratory antigen.
WO200155448-A1.
                                                                                                                                                                                                                                          ABL98499 standard; DNA; 15518 BP.
Human testicular antigen encoding DNA fragment SEQ ID NO: 3151
WO200155317-A2.
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24.4PR-2003.
(HUMA-) HUMAN GENOME SCI INC.
6ry Match
5.9%; Score 109; DB 11; Length 32146;
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ry Match

t Local Similarity 79.9%; Pred. No. 1e-22;
                                                                                                      AALOS935 standard; DNA; 15518 BP.
Human reproductive system related antigen DNA SEQ ID NO: 8623.
WO200155320-A2.
02-AUG-2001.
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                                                           Length 15517;
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Best Local Similarity 79.9%; Pred. No. 1e-22;
RESULT 1114
ID ADG41564 standard; DNA; 32248 BP.
DE Human respiratory system associated genomic DNA seq id 802.
PN US2003215893-A1.
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(HUMA-) HUMAN GENOME SCI INC.
(HTWA-) HUMAN GENOME SCI INC.
5.9%; Score 109; DB 4;
(ery Match milarity 79.9%; Pred. No. 8.8e-23;
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                 02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
Ery Match 5.9%; Score 109; DB 4;
ery Match 76.7%; Pred. No. 6.5e-23;
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17 Match

1. Local Similarity 76.7%; Pred. No. 6.5e-23;
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(HUMA-) HUMAN GENOME SCI INC.
5.9%; Score 109; DB 4
ery Match 5.9%; Pred. No. 1e-22;
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(HUMA-) HUMAN GENOME SCI INC.
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...a.) HUMAN GENOM.
...a.Y Match
Best Local Similarity 7
RESULT 1110
ID AA228363 stand?
DE Genomic ser
PN WO20015
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Loy Match
Best Local Similarity RESULT 1107
ID AALOS335 stander
DE Human represent PN W02001er
PD 02-7
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Best Local Similarity
RESULT 1112
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Best Local Similarity
RESULT 1113
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                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1109
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AAK76172 standard; DNA; 34435 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30984.
WO200157182-A2.
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23335.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 108.8; DB 10; Length 44325; 76.1%; Pred. No. 1.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uuery Match 5.9%; Score 108.8; DB 11; Length 2837; Best Local Similarity 79.5%; Pred. No. 2.7e-23; RESULT 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 44325;
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5.9%; Score 109; DB 13; Length 94001;
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PD 24-APR-2003.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 5.9%; Score 109; DB 11; Length 32248;

Best Local Similarity 79.9%; Pred. No. 1e-22;

RESULT 1116
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Human DADI carcinoma associated gene, SEQ ID NO:1478.
WO2003057146-A2.
                                                                                                                                                                                                                                                                            RESULT 1117
ID AD33491 standard, DNA; 94001 BP.
DE Human LAR related nucleotide sequence SEQ ID NO:20
PN WO2004010956-A2.
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PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

Query Match 5.9%; Score 108.8; DB 6;

Best Local Similarity 79.2%; Pred. No. 2e-23;

RESULT 1120
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(HUMA-) HUMAN GENOME SCI INC.
Guery Match
5.9%; Score 108.8; DB 4;
Best Local Similarity 79.2%; Pred. No. 1e-22;
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Pred. No. 1.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.9%; Score 108.8; DB 5; 79.5%; Pred. No. 9.9e-24;
                                                                                                                                                                                      09-AUG-2001.
(HUWA-) HUMAN GENOME SCI INC.
5.9%; Score 109; DB 4;
FLocal Similarity 79.9%; Pred. No. 1.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABV46377 standard; cDNA; 556 BP.
Human prostate expression marker cDNA 46368.
WO200160860-A2.
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Query Match 5.9%; Score 108.8; 1
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Human cDNA of the invention SEQ ID NO:2282.
EP1347046-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABA96807 standard; cDNA; 1777 BP. Human uteroglobin 9-encoding cDNA.WO200198337-A1.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Dadl genomic sequence.
WO2003045230-A2.
05-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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Query Match
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                                                                                                                                                                                                                                                                                                       Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAL37255 standard; DNA; 4140 BP.
Human musculoskeletal system related polynucleotide SEQ ID NO 3620.
WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human musculoskeletal system-associated genomic DNA - SBQ ID 3620.
US2004009488-A1.
                                                                                                                                                                                                                                                                                                                           PD 22-JUL-2004.

PA (SAGR-) SAGRES DISCOVERY INC.

Query Match

Best Local Similarity 74.6%; Pred. No. 2.7e-22;

RESULT 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 108.6; DB 10; Length 167163; Pred. No. 3.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 110000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.9%; Score 108.6; DB 12; Length 25899; 80.2%; Pred. No. 1.2e-22;
                    5.9%; Score 108.8; DB 10; Length 44325; 76.1%; Pred. No. 1.4e-22;
                                                                                                                                                                                                               Query Match 5.9%; Score 108.8; DB 12; Length 44325; Best Local Similarity 76.1%; Pred. No. 1.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
ry Match
t Local Similarity 80.2%; Pred. No. 3.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 108.6; DB 8; Length 65464; Pred. No. 2.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABX60243 standard; cDNA; 4140 BP. cDNA encoding novel human musculoskeletal system antigen #2587. US2002147140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
Ery Match 5.9%; Score 108.6; DB 4; Length 4140;
ery Match similarity 80.2%; Pred. No. 3.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.9%; Score 108.6; DB 8; Length 4140; 80.2%; Pred. No. 3.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ59374 standard; DNA; 25899 BP.
Human cancer-associated (CA) gene sequence SEQ ID NO:10.
WO2004058288-A1.
                                                                                                                                                                                                                                                                          ADQ97651 standard; DNA; 127943 BP.
Human cancer associated sequence HD10-021, SEQ ID 628.
WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABX13172 standard; DNA; 65464 BP.
Human gene encoding a Noelin-1-like secreted protein.
US2002173459-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 108.6; DB 12;
Pred. No. 2.9e-22;
                                                                         ADM74555 standard; DNa; 44325 BP.
Human carcinoma associated (CA) nucleic acid #112.
US2004072154-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE82948 standard; DNA; 167163 BP.
Human PVT1 genomic DNA sequence.
WO2003080808-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ30993 standard; DNA; 4140 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
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Best Local Similarity 77.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-2003.
(SAGR-) SAGRES DISCOVERY.
Query Match 5.9
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                            15-APR-2004.
(MORR/) MORRIS D W.
(ENGE/) ENGELHARD E K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
RESULT 1132
Query Match
Best Local Similarity
RESULT 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
RESULT 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD 10-OCT-2002.

PA (ROSE)/ ROSEN C A.

R (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.

Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1131
                 Query Match
Best Local Similarity
RESULT 1125
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(PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-2004
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#ESULT 1138

D AB02754 standard; DNA; 62124 BP.

DE Human cancer-associated genomic DNA HD16-028.

PN W02004074320-A2.

PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.

Query Match

BEST Local Similarity 79.5%; Pred. No. 2.4e-22;

RESULT 1139

ID ADG86768 standard; DNA; 104245 BP.

DE Human cancer-associated genomic Consequence of the consequence of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK67282 standard; DNA; 33147 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-DEC-2003.
(ISIS-) ISIS PHARM INC.
| Secore 108.4; DB 12; Length 104245; | Secore 108.4; DB 12; Length 104245; | Secore 108.4; DB 12; | Secore 1045; | Secore 104.5; | Secor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 5.9%; Score 108.4; DB 13; Length 107745; Local Similarity 78.2%; Pred. No. 3.3e-22;
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(HUMA-) HUMAN GENOME SCI INC.
6-ry Match
5.9%; Score 108.4; DB 4; Length 32194;
st Local Similarity 79.5%; Pred. No. 1.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMAN) GENOME SCI INC.
5.9%; Score 108.4; DB 4; Length 33147;
it Local-Similarity 77.9%; Pred. No. 1.6e-22;
AADSB742 standard; DNA; 20733 BP.
Human transmembrane serine protease (TSP1-TSP34) gene fragment
WO2003064641-Al.
                                                                                                                                                                                                                                                                                                                                                                 Length 20733;
                                                                                                                                                                                                                                Best Local Similarity 79.8%; Score 108.4; DB 9; Length 2073; RESULT 1135

ID AAL04340 standard; DNA; 32194 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7028. PD 02-8005-320-A2.
PD 02-8003-2001.
PA (HUMA-) HTMAN.
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Renal cell carcinoma differentially expressed gene #322.
W0200408933-A2.
10-JUN-2004.
(AMHP ) WYETH.
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Human cancer-associated (CA) gene HD07-040.
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Human PPAR-delta DNA fragment SEQ ID 4.
US2004063129-A1.
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Human GPCR gene SEQ ID NO:883.
EP1270724-A2.
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(SAGR-) SAGRES DISCOVERY INC.
gry:Match 5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 1137
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RESULT 1140
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(GAAR/) GAARDE W.
(FREI/) FREIER S M
(WATT/) WATT A T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004058146-A2.
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Query Match
Best Local Similarity
RESULT 1151
ID ADC86642 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 21-MAY-2004.

PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.

PA (UNIV-) UNIVERSITAETSKLINIKUM FREIBURG.

Query Match 5.9%; Score 108.4; DB 12; Length 300001;

Best Local Similarity 78.2%; Pred. No. 6.2e-22;

RESULT 1145
                                                                                                                                    5.9%; Score 108.4; DB 12; Length 170245; 66.7%; Pred. No. 4.4e-22;
                                                                                                                                                                                                                                                        10-APR-2003.
(MOUN ) MOUNT SINAI SCHOOL MEDICINE.
(MOUN ) MOUNT SINAI SCHOOL MEDICINE.
5.9%; Score 108.4; DB 10; Length 300000;
cry Match 78.2%; Pred. No. 6.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                               Human protein tyrosine phosphatase 11 gene sequence SEQ ID NO:33 WO2004041216-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD 18-DEC-2003.

PA (1S.1S-) ISIS PHARM INC.

Query Match 5.9*; Score 108.2; DB 12; Length 28001;

Best Local Similarity 78.8*; Pred. No. 1.7e-22;

RESULT 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-2003.
(ISIS-) ISIS PHARM INC.
Query Match 5.9%; Score 108.2; DB 12; Length 28001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.9%; Score 108.2; DB 12; Length 28001; 78.8%; Pred. No. 1.7e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABĀ17986 standard; DNA; 4850 BP.
Human nervous system related polynucleotide SEQ ID NO 10317.
WO200159063-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HG-AUG-2001.

(HUMA-) HUMAN GENOME SCI INC.

Ery Match

S.9%; Score 108.2; DB 5;

ery Match

74.4%; Pred. No. 5.8e-23;
                                                                                                                                                    Best Local Similarity 66.7%; Fred. No. 4.4e-22; RESULT 1143

ID ADBESTS standard; DNA; 300000 BP.

B. Human PTPN11 genomic DNA sequence SEQ ID NO:33.

PN WO2003029422-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADI36730 standard; DNA; 28001 BP.
Genomic DNA sequence #2 encoding human KOX 1.
US2003232438-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI36729 standard; DNA; 28001 BP.
Genomic DNA sequence #1 encoding human KOX 1.
US2003232438-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM93170 standard; cDNA; 28001 BP.
Human KOX-1 variant cDNA sequence.
US2004087536-A1.
                                                                                                                                                                                                                                                                                                                                                                             ADO14076 standard; DNA; 300001 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM93169 standard; DNA; 28001 BP.
Human KOX-1 genomic sequence.
US2004087536-A1.
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Human genomic sequence hCG33132.
WO2003073826-A2.
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                         ᇤᇽ
  TWINE N C.
BURCZYNSKI M E
TREPICCHIO W I
                                                               (DORN/) DORNER A.
(STOV/) STOVER J A.
(SLON/) SLONI D K.
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DOBI/) DOBIE K W. (FREI/) FREIER S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DOBI/) DOBIE K W. (FREI/) FREIER S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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Best Local Similarity
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                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                               Query Match
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ID ADM93170
DE Human KC
PN US200408
PD 06-MAY-
PA (DOBI/)
PA (FREI/)
                                               (TREP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1150
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5.9%; Score 108; DB 4; Length 51469;

Jour 1156

ID AAK6932 standard; DNA; 51469 BP.

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24134.

PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Ouery Match

Best Local Similarity 78.2%; Pred. No. 2.86-22;

RESULT 1157

ID ADE24797 standard; DNA; 186510 BP.

PN US2003143544-A1.

PN US2003143544-A1.

PD 31-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK78813 standard; DNA; 51469 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33625
                                                                                                                                                                                            Length 349881;
5.9%; Score 108.2; DB 11; Length 45814; 78.8%; Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 186510;
                                                                                                                                                                                                                                                                                                                                                               Length 32249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

QUETY MATCh 5.9%; Score 108; DB 5; Length 32249;

Best Local Similarity 83.5%; Pred. No. 2.1e-22;

RESULT 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(ery Match 5.9%; Score 108; DB 4; Length 51469;
ery Match 78.2%; Pred. No. 2.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Length 534;
                                                                                                                                                                                                                                                              PD 02-MUG-2001.

PD (HUMA-) HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 83.5%; Pred. No. 2.1e-22;

RESULT 1153

ID AAIG3718 standard; DNA; 32249 BP.

PW W020155323-A2.

PD 02-AUG-2001.

PD 02-AUG-2001.
                                                                                                                                                                                                                                        AA199368 standard; DNA; 32249 BP.
Human excretory related polynucleotide SEQ ID NO 1132.
WO200155313-A2.
                                                                                                                                  PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

Query Match 5.9%; Score 108.2; DB 10;

Best Local Similarity 75.8%; Pred. No. 7.9e-22;

RESULT 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 108; DB 10;
Pred. No. 6.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 107.8; DB Pred. No. 2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
SEQ ID NO:6026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate expression marker cDNA 16570.
WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE. INC.
                                            Human GPCR gene SEQ ID NO:1095.
EP1270724-A2.
02-7AN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vecty recommendation 78.2%; Pred RESULT 1155
ID AAK70270 standard; DNA; 51469 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.5%; Pr
RESULT 1158
ID AAH09191 standard; CDNA; 534 BF
DE Human CDNA clone (3'-primer) SF
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 79.1%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABV16579 standard; cDNA; 537
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WO200281657-A2.
                                                                      02-AUG-2001
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                                                                                                                                                                                                                02-AUG-2001
                                                                                                                                                                                                                                                   Query Match
                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAL51575 standard; DNA; 4272 BP.
Human nucleic acid-associated protein coding sequence - SEQ ID No 58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24042 WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL35859 standard; DNA; 9439 BP.
Human musculoskeletal system related polynucleotide SEQ ID NO 2224.
WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.9%; Score 107.8; DB 10; Length 3887; 71.1%; Pred. No. 6.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.9%; Score 107.8; DB 13; Length 647; 51.8%; Pred. No. 2.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.9%; Score 107.8; DB 4; Length 5335; 79.1%; Pred. No. 8.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4272;
                                                                    5.9%; Score 107.8; DB 5; Length 537; 79.0%; Pred. No. 2e-23;
                                                                                                                                                                                                                                 6; Length 546;
                                                                                                                                                                                                                                                                                                                                                                        5.9%; Score 107.8; DB 5; Length 621; 74.7%; Pred. No. 2.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Length 9439;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel canine microarray-related DNA sequence SeqID4731
WO2004063324-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA199373 standard, DNA, 9439 BP.
Human excretory related polynucleotide SEQ ID NO 1137.
WO200155313-A2.
                                                                                                                      ABN62103 standard; cDNA; 546 BP.
Human cancer related polynucleotide SEQ ID NO 2070.
WO200214500-A2.
21-FEB-2002.
                                                                                                                                                                                                                                                                               AAS90974 standard; cDNA; 621 BP.
DNA encoding novel human diagnostic protein #26778
WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.9%; Score 107.8; DB 8; 74.7%; Pred. No. 7.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD72114 standard; cDNA; 3887 BP.
Human endozepine-like protein NOV1a cDNA NOV1a.
US2003195149-Al.
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ry Match
5.9%; Score 107.8; DB 4
1. Local Similarity 74.7%; Pred. No. 1.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.9%; Score 107.8; DB 479.1%; Pred. No. 3.9e-23
                                                                                                                                                                                                                               5.9%; Score 107.8; DB 81.2%; Pred. No. 2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cDNA sequence SEQ ID NO:18381.
EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH18351 standard; cDNA; 1579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK69230 standard; DNA; 5335 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                              ADQ53429 standard; DNA; 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENE LOGIC INC. (PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST.
Lry Match

Jest Local Similarity

RESULT 1160

ID ABN62103 standar

DE Human cancer

PN WO200214<sup>e</sup>

PD 21-FF<sup>e</sup>

PA (r<sup>e</sup>

PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1163
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Best Local Similarity
RESULT 1168
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RESULT 1162
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RESULT 1165
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                                                                                                                                                                                                                                        Best Local Similarity
RESULT 1161
                                                                                                                                                                                                                                                                                                                               11-OCT-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003000864-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2001
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ADJ08557 standard; DNA; 17397 BP.
Human cardiovascular system associated polypeptide-related DNA SeqID1945.
US2004005575-Al.
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Human musculoskeletal system-associated genomic DNA - SEQ ID 2224.
US2004009488-A1.
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(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI SCORE 107.8; DB 10; Length 17397;
(ery Match similarity 74.7%; Pred. No. 1.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 107.8; DB 10; Length 14800;
Pred. No. 1.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME 5.9%; Score 107.8; DB 4; Length 19334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 17397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IS-JAN-2004.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.9%; Score 107.8; DB 12; Length 9439;
ery Match 74.7%; Pred. No. 1.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cardiovascular system antigen genomic DNA SEQ ID No 1945.
WO200155321-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 17397;
                                                                                                                                                                                                                                                                                ABXS8847 standard; cDNA; 9439 BP.
cDNA encoding novel human musculoskeletal system antigen #1191.
US2002147140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cardiovascular system antigen genomic DNA SEQ ID No 1943.
WO200155321-A2.
                            DB 4; Length 9439;
                                                                                                                                                                                                               Length 9439;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cardiovascular system related genomic DNA #705.
US2003059908-A1.
                                                                                              AAI63723 standard; DNA; 9439 BP.
Human kidney related polynucleotide SEQ ID NO 1038
WO200155323-A2.
                                                                                                                                                                                     (HUMAN) HUMAN GENOME SCI INC.

ry Match 5.9%; Score 107.8; DB 5;

t Local Similarity 74.7%; Pred. No. 1.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 107.8; DB 8;
Pred. No. 1.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN GENOME SCI INC.
h 5.9%; Score 107.8; DB 4;
Similarity 74.7%; Pred. No. 1.7e-22;
HUMAN GENOME SCI INC.
1.9%; Score 107.8; DB 4.
Similarity 74.7%; Pred. No. 1.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JAN-2004.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.9%; Score 107.8; DB 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABV75863 standard; DNA; 14800 BP.
Human potassium channel transporter gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS36443 Btandard; DNA; 19334 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS36445 standard; DNA; 17397 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE47139 standard; DNA; 17397 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY.

(WEIMA) WEI M.

(KETC) KETCHUM K A.

(DFRA/) DI FRANCESCO V.
                                             Best Local Similarity RESULT 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                          (BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          (ROSE/) ROSEN C A. (RUBE/) RUBEN S M.
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WO200224747-A2.
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US2004005575-A1.
US2004005575-A1.
US-JAN-2004.
(HUMA-) HUMAN GENOME SCI INC.
5.9%; Score 107.8; DB 13; Length 19345; St. Local Similarity 74.7%; Pred. No. 1.8e-22;
                                                                                                                                                                                                                       Human cardiovascular system associated polypeptide-related DNA SeqID1943 US2004005575-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB16928 standard; DNA; 49939 BP.
Human DYXC1 DNA, chromosomal gene region nucleotides 100001-150000.
WO2003068814-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISSE-) ISIS PHARM INC.

ry Match

5.9%; Score 107.8; DB 12; Length 29001;

t Local Similarity 74.7%; Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB79960 standard; DNA; 62805 BP.
Human kinase protein encoding genomic DNA SEQ ID NO:3.
ery Match
5.9%; Score 107.8; DB 10; Length 62805;
st Local Similarity 79.1%; Pred. No. 3.7e-22;
                                                                                                                                              5.9%; Score 107.8; DB 10; Length 19334; 74.7%; Pred. No. 1.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 59856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 19345;
                                                                                                                                                                                                                                                                                                             Length 19334
                                                                                                                                                                                                                                                                                                                                                                                                                       02-40G-2001.
(HUMA-) HUMAN GENOME SCI INC.
Ery Match
Fry Match
From Similarity 74.7%; Pred. No. 1.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 107.8; DB 9; Length 49939; 79.1%; Pred. No. 3.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                        Human cardiovascular system antigen genomic DNA SEQ ID No 1944 WO200155321-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK94411 standard; DNA; 109906 BP.
DNA encoding endothelin converting enzyme 1 (ECE-1) #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE47138 standard; DNA; 19345 BP.
Human cardiovascular system related genomic DNA #704.
US2003059908-A1.
                                                              Human cardiovascular system related genomic DNA #703
US2003059908-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 107.8; DB 11;
Pred. No. 3.6e-22;
                                                                                                                                                                                                                                                                                                        5.9%; Score 107.8; DB 13; 74.7%; Pred. No. 1.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-2003.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
6ry Match
5.9%; Score 107.8; DB 10
    74.7%; Pred. No. 1.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 74.7%; Pred.
RESULT 11816
ID ADD0855 standard; DNA; 19345 BP.
DE Human cardiovascular system associae
PD 08-JAN-2004.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADO85575 standard; DNA; 29001 BP. Human zinedin polynucleotide. US2004110701-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACN44290 standard; DNA; 59856 BP. Human genomic sequence hCG24994. W02003073826-A2.
                                                                                                                                                                                                      ADJ08555 standard; DNA; 19334 BP
                                           ADE47137 standard; DNA; 19334 BP
                                                                                                                                                                                                                                                                                                                                                                   AAS36444 standard; DNA; 19345 BP
                                                                                                  27-MAR-2003.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
RESULT 1177
ID ADB47137 standard; DN
DE Human cardiovascular
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-AUG-2003.
(LICN ) LICENTIA LTD.
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Best Local Similarity
RESULT 1184
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SULT 1185
                                                                                                                                                              Local Similarity
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Best Local Similarity
RESULT 1180
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RESULT 1186
ID ABK94411 standard; ID
DE DNA encoding endothe
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                Query Match
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Genomic sequence #169 encoding novel human connective tissue polypeptide. WO200155343-A1.
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Genomic sequence #204 encoding for novel human respiratory antigen.
WO200155448-A1.
                                                                                                                                                                                                                                                                                        5.9%; Score 107.8; DB 13; Length 110000; 79.1%; Pred. No. 5.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 107.6; DB 11; Length 152330; Pred. No. 7.4e-22;
                                                                                                                                                                                                                       DB 12; Length 109906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 101616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) 09-MAR-2001.

1 (CNRS) CNRS CENT NAT RECH SCI.

5.8%; Score 107.6; DB 5; Length 110000;

Best Local Similarity 80.1%; Pred. No. 6.1e-22;
                                     5.9%; Score 107.8; DB 6; Length 109906; 79.1%; Pred. No. 5.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 21470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.8%; Score 107.4; DB 11; Length 2553; 71.3%; Pred. No. 7.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%; Score 107.6; DB 4; Length 21470; 78.4%; Pred. No. 2.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vuery match 5.8%; Score 107.4; DB 6; Length 397; Best Local Similarity 79.4%; Pred. No. 2.3e-23; RESULT 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL84412 standard; cDNA; 397 BP.
Human ovarian cancer related cDNA clone SEQ ID NO:7390.
WO200192581-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.8%; Score 107.6; DB 11; 80.1%; Pred. No. 5.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USCUCZ-2003.
USCUCZ-2003.
(HUMA. - HUMAN GENOME SCI INC.
(HUMA. - HUMAN GENOME SCI INC.
5.8%; Score 107.6; DB 9;
Lery Match
- Similarity 78.4%; Pred. No. 2.2e-22;
                                                                                                                                                                                                                     5.9%; Score 107.8; DB 1; 79.1%; Pred. No. 5.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF84800 standard; DNA; 110000 BP.
Nucleotide sequence of the human SPG4 gene.
FR2798138-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADM02993 standard; cDNA; 2553 BP.
Human cDNA of the invention SEQ ID NO:1678.
EP1347046-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Connective tissue related genomic DNA #169. US2003054375-A1.
                                                Best Local Similarity 79.1%; Pred. No. 5.2
RESULT 1187
DE Human gene associated with low HDL-C ECEI.
PN US2004043389-Al.
28-MAR-2002.
(EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1193
ID ACN45070 standard; DNA; 152330 BP.
DE Human genomic sequence hCG32392.
PN WO2003073826-A2.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                         DNA; 21470 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB60426 standard; DNA; 21470 BP
                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 78.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                         04-MAR-2004.
(VITI-) VITIVITY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-DEC-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                     Best Local Similarity
RESULT 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1190
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Best Local Similarity
RESULT 1191
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                                                                                                                                                                                                                                                                                                                                                       ABK42270 standard;
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5.8%; Score 107.2; DB 6; Length 1679; 68.9%; Pred. No. 6.3e-23;
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Human FLAP genomic DNA SEQ ID NO:1
WO2004035741-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC86168 standard; DNA; 21704 BP.
Human GPCR gene SEQ ID NO:621.
EP1270724-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABQ77404 standard; DNA; 78025 BP.
Human SELP DNA.
WO2003016494-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS55783 standard; cDNA; 1621 BP
                                                                                                                                                                                                     (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-SEP-2004.
(SAGR-) SAGRES DISCOVERY INC.
 Luery Match
Best Local Similarity to RESULT 1206
ID ADM0234 stand DE Human cDNA
PN EP1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-FEB-2003.
(VITI-) VITIVITY INC.
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Best Local Similarity
RESULT 1212
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Human respiratory system associated polypeptide-related DNA SeqID798.
US2003077704-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAK82098 standard; DNA; 46366 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36910.
WO200157182-A2.
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34249.
WO200157182-A2.
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Pred. No. 1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vuery Match 5.8%; Score 107.4; DB 13; Length 87847;
Best Local Similarity 69.2%; Pred. No. 6.1e-22;
RESULT 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.8%; Score 107.4; DB 12; Length 202100; 77.5%; Pred. No. 1e-21;
                                                                                                                                                                                                                                                                                                                            24-ADR-2003.
24-MDR-2003.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
5.8%; Score 107.4; DB 11; Length 17498;
iery Match
79.4%; Pred. No. 2.3e-22;
                                                                                                                                                                                                                       5.8%; Score 107.4; DB 10; Length 17498; 79.4%; Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
ry Match
t Local Similarity 76.3%; Pred. No. 4.2e-22;
                                                                   5.8%; Score 107.4; DB 4; Length 17498; 79.4%; Pred. No. 2.3e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.8%; Score 107.2; DB 4; Length 708;
                                                                                                                     ADG41560 standard; DNA; 17498 BP.
Human respiratory system associated genomic DNA seg id 798.
US2003215893-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL51168 standard; cDNA; 1679 BP.
Peroxidase-related protein 12-21 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human IDE/ KNSL1 genomic sequence, SEQ ID 484. WO2003054143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABD33066 standard; DNA; 87847 BP.
Human cancer-associated genomic DNA HD23-013.
WO2004074320-A2.
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10-APR-2002.
(BODE-) BODE GENE DEV CO LTD SHANGHAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE43315 standard; DNA; 202100 BP
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                                                                                                                                                                             20-NOV-2003.
(HUMA-) HUMAN GENOME SCI INC.
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(SAGR-) SAGRES DISCOVERY INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-2003.
(GEHO ) GEN HOSPITAL CORP.
Best Local Similarity
RESULT 1197
ID ADG41560 standa
DE Human respr
PN US20037
PD 20
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Best Local Similarity
RESULT 1199
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Best Local Similarity
RESULT 1202
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Best Local Similarity
RESULT 1203
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Best Local Similarity
RESULT 1204
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RESULT 1205
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/AAK66092 standard; DNA; 9454 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23904.
WO200157182-A2.
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23905.
WO200157182-A2.
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PA (DECO-) DECODE GENETICS EHF.

0.ery Match

Best Local Similarity 80.4%; Pred. No. 8.2e-22;

RESULT 1213

ID ADS94372 standard; DNA; 398800 BP.

DE Human 5-lipoxygenase activating protein (FLAP) gene.

PN WO2004035746-A2.

PD 29-APR-2004.

PA. (DECO-) DECODE GENETICS EHF.

S.8%; Score 107.2; DB 13; Length 110000;

RESULT.

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Best Local Similarity 70.8%; Pred. No. 6.6e-22;
RESULT 1211
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ry Match
t Local Similarity 80.4%; Pred. No. 2.6e-22;
                                                                                                                                                                                                                                                                                                                        5.8%; Score 107.2; DB 11; Length 2455; 75.7%; Pred. No. 8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 107.2; DB 4; Length 9454;
Best Local Similarity 80.4%; Pred. No. 1.88-22;
RESULT 1208
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ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
EY MAtch
Local Similarity 77.1%; Pred. No. 3e-22;
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Human cancer-associated genomic DNA HD16-030.
WO2004074320-A2.
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ADM02334 standard; cDNA; 2455 BP.
Human cDNA of the invention SEQ ID NO:1019.
EP1347046-A1.
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(BODE-) BODE GENE DEV CO LTD SHANGHAI
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK42490 standard; DNA; 7359 BP.
Genomic sequence #389 encoding novel human connective tissue polypeptide.
WO200155343-A1.
                                                                                                                                                                                                                                                                                                                                             ABK42489 standard; DNA; 7359 BP.
Genomic sequence #388 encoding novel human connective tissue polypeptide.
WO200155343-A1.
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WO200157182-A2.
09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK69061 standard; DNA; 7359 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23873.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL97456 standard; DNA; 7625 BP.
Human testicular antigen encoding DNA fragment SEQ ID NO: 2108.
WO200155317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AALO4533 standard, DNA, 7625 BP.
Human reproductive system related antigen DNA SEQ ID NO: 7221.
WO20<u>01</u>55320-A2.
                                                                                                                                     Genomic sequence #330 encoding novel human enzyme polypeptide. WO200155301-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
5.8%; Score 107; DB 4; Length 7625;
             Length 1621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 7359;
                                                                                                                                                                                                                                                                          Length 6437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 7359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 7359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 7359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 7359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 7359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lunh #389.

Lucry Match
Best Local Similarity 79.7%; Pred. No. 1.8e-22;
RESULT 1221
ID ADB6645 standard; DNA; 7359 BP.
DE Connective tissue related operance of the connective tissue ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HTMA-) HUMAN GENOME SCI INC.
(ery Match 5.8%; Score 107; DB 4;
          5.8%; Score 107; DB 6; 76.5%; Pred. No. 7.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%; Score 107; DB 4; 79.7%; Pred. No. 1.8e-22;
                                                                                                                                                                                       02-40G-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
5.8%; Score 107; DB 4;
(ery Match 1.7e-22;
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ry Match
t Local Similarity 79.7%; Pred. No. 1.8e-22;
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ry Match
5.8%; Score 107; DB 4;
t Local Similarity 79.7%; Pred. No. 1.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
ry Match
t Local Similarity 79.7%; Pred. No. 1.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.8%; Score 107; DB 4; 78.0%; Pred. No. 1.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADB66646 standard; DNA; 7359 BP.
Connective tissue related genomic DNA #389.
US2003054375-A1.
                                                                                                       AAS42014 standard; DNA; 6437 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK69062 standard; DNA; 7359 BP
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(HUMA-) HUMAN GENOME SCI INC.
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Query Match 5.8%;
Query Match
Best Local Similarity
RESULT 1215
ID AAS42014 standard; DN
DE Genomic sequence #33C
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1220
ID ADB66646 standard; DN
DE Connective tissue rel
PN US2003054375-A1.
PD 20-WAR-2003.
PA (HUMA-) HUMAN GENOME
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                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 1217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1218
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ABLÉSR38 standard; DNA, 39265 BP.
Polynucleotide sequence related to an analgesic peptide-like structure.
WO200204642-A1.
                                                                                                                                                                                                                                    Human digestive system antigen genomic sequence SEQ ID NO: 4840 WO200155314-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUL-2003.
(INCY-) INCYTE GENOMICS INC.
5.8%; Score 107; DB 10; Length 173805;
st Local Similarity 79.7%; Pred. No. 1.3e-21;
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                                                              Length 57013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 39265;
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                                                                                                                                                                                                                                                                                                                    Length 28563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADLI3775 standard; DNA; 173805 BP.
Osteoarthritis-associated polymorphic nucleotide #307.
WO2003054166-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO. 
INTY MATCH 5.8%; SCORE 107; DB 10; 
It Local Similarity 79.7%; Pred. No. 9.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.8%; Score 107; DB 11;
Best Local Similarity 79.7%; Pred. No. 6.3e-22;
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Pred. No. 9.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                  PD 17-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 107; DB 6;
Best Local Similarity 78.0%; Pred. No. 5.1e-22;
RESULT 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 107; DB 10;
Pred. No. 9.5e-22;
Best Local Similarity 78.0%; Pred. No. 1.9e-22; RESULT 1224
                                                                                                                                                                                                                                                                     02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
F.8%; Score 107; DB 4;
lery Match 5.0%; Pred. No. 4.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABD33453 standard; DNA; 51837 BP.

Human cancer-associated (CA) gene HD07-086.

W02004058146-A2.

15-JUL-2004.

15-JUL-2004.

5.8*; Score 107; DB 13 et Local Similarity 78.0%; Pred. No. 6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene #420 used to diagnose liver cancer WO200229103-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC87336 standard; DNA; 108316 BP.
Human GPCR gene SEQ ID NO:1789.
EP1270724-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACN45046 standard; DNA; 57013 BP. Human genomic sequence hCG39345. WO2003073826-A2.
                                                                                                                                                                                                                     AAK91264 standard; DNA; 28563 BP.
                                                       AAS42015 standard; DNA; 9742 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2002. (GENE-) GENE LOGIC INC.
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Best Local Similarity
RESULT 1234
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 1226
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ADM47750 standard; DNA; 8270 BP.
NOV14 coding sequence, SEQ ID 47.
WO200268647-A2.
               ADH47720 standard; DNA; 8250 BP. NOV3b coding sequence, SEQ ID 17. WO200268647-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1243
ID ADL25633 standard, DNA, 8270 BP.
DE Human diagnostic gene, NOV14.
PN US2004005557-A1.
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PENA C B A.
TCHERNEV V T.
ZERHUSEN B D.
MILLET I.
MILLET G E.
LEPLEY D M.
SMITHSON G.
BAUMGARTHER D
BERRMANN J L.
                                                                                                                                                                              17-OCT-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLMAN S D.
SPYTEK K A.
BOLDOG F L.
VERNET C A M.
                                                             06-SEP-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                   11-DEC-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                     A (CURA-) CURAGEN CORP. Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
RESULT 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GUO X.
EDINGER S R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATTURAJAN M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHENOY S G.
CASMAN S J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MALYANKAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEYM/)
(GORM/)
(MEZE/)
(KEKU/)
    RESULT 1238
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22626.
WO200157182-A2.
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Pred. No. 2.3e-22;
                                        22-OCT-1998.
(GEMY) GENETICS INST INC.
5.8%; Score 106.8; DB 2; Length 2754;
ery Match
5.8%; Pred. No. 1.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                     O'-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.8%; Score 106.8; DB 4; Length 5289;
ery Match 79.0%; Pred. No. 1.7e-22;
                                                                                                                                                                                                                                                                                                5.8%; Score 106.8; DB 6; Length 2754; 79.0%; Pred. No. 1.2e-22;
AAV62746 btandard; cDNA; 2754 BP.
Human secreted protein clone en539_8 cDNA.
WO9846757-A2.
                                                                                                                  ABQ92049 standard; cDNA; 2754 BP.
Human polynucleotide SEQ ID NO 46.
US2002065394-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADL25603 standard; DNA; 8249 BP. Human diagnostic gene, NOV3b.
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                                                                                                                                                                      JACOBS K.

MCCOY J M.

LAVALLIE B R.

COLLINS-RACIE L A.

EVANS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZERHUSEN B D.
MILLET I.
MILLET C E.
LEPLEY D M.
SMITHSON G.
BAUMGARTNER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLMAN S D.
SPYTEK K A.
BOLDOG F L.
VERNET C A M.
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PATTURAJAN M.
                                                                                                                                                                                                                                                    (MBRB/) MERBERG D.
(TREA/) TREACY M.
(SPAU/) SPAULDING V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HERRMANN J L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHERNEV V T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ROTH/) ROTHENBERG M.
(STON/) STONE D J.
(BURG/) BURGESS C E.
                                                                        Query Match
Best Local Similarity
RESULT 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GUO X.
EDINGER S R.
MACDOUGALL J
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 1236
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LI L.
SHENOY S G.
CASMAN S J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAUPIER R J. GERLACH V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEYMAN J A.
SORMAN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PADIGARU M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELLERMAN K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEZES P D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2004005557-A1.
                                                                                                                                                                                          (MCCO/)
(LAVA/)
(COLL/)
(EVAN/)
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uuery Match 5.8%; Score 106.8; DB 11; Length 8250;
Best Local Similarity 75.9%; Pred. No. 2.3e-22;
RESULT 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 5.8%; Score 106.8; DB 12; Length 8250; Local Similarity 75.9%; Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 5.8%; Score 106.8; DB 11; Length 8270; Local Similarity 75.9%; Pred. No. 2.3e-22;
Query Match 5.8%; Score 106.8; DB 6; Length 8250; Best Local Similarity 75.9%; Pred. No. 2.3e-22; RESULT 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%; Score 106.8; DB 6; Length 8270; 75.9%; Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP68285 standard, DNA; 8270 BP.
Human NOV14a DNA encoding a B7-H2 like protein SeqID 47
WO200281510-A2.
                                                                                                   ADP68256 standard; DNA; 8250 BP.
Human NOV3b DNA encoding a B7-H2 like protein SeqID 17.
WO200281510-A2.
                                                                                                                                                                                                                                                                                                                                                           ADH71873 standard; DNA; 8250 BP.
Human gene of the invention NOV31a SEQ ID NO:769.
WO2003102155-A2.
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WO2003054143-A2.
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                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                 AAL16871 standard; DNA; 15745 BP.
Human musculoskeletal system related polynucleotide SEQ ID NO 3236.
WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ30609 standard; DNA; 15745 BP.
Human musculoskeletal system-associated genomic DNA - SEQ ID 3236.
US2004009488-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 106.8; DB 12; Length 15745;
Best Local Similarity 79.0%; Pred. No. 3.4e-22;
RESULT 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 63824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 29360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 63045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 20000;
                                                                                                                                                             5.8%; Score 106.8; DB 12; Length 8270; 75.9%; Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.8%; Score 106.8; DB 8; Length 15745; 79.0%; Pred. No. 3.4e-22;
                                                                                                                                                                                                                                                                                                                  Length 15745;
                                                                                                                                                                                                                                                                                                                                                                      ABX50859 standard; cDNA; 15745 BP.
cDNA encoding novel human musculoskeletal system antigen #2203.
US2002147140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A truncated portion of DNA encoding human kinesin-like 1. US2004180847-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADQ97189 standard; DNA; 29360 BP.
Human cancer associated sequence HD08-012, SEQ ID 165.
WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE43743 standard; DNA; 63824 BP. Polymorphic human KNSL1 genomic sequence, SEQ ID 348.
                                                                                                                                                                                                                                                                     G2-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
6-ry Match
5.8%; Score 106.8; DB 4;
6-ry Match
79.0%; Pred. No. 3.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 106.8; DB 10;
Pred. No. 7.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SACUL-2004.
(SACR-) SAGRES DISCOVERY INC.
(Ery Match
6-19 Actor o'milarity 79.0%; Pred. No. 4.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%; Score 106.8; DB 1 75.9%; Pred. No. 3.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%; Score 106.8; DB 1
82.6%; Pred. No. 7.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1250
ID ADEA13742 Standard; DNA; 63824 BP.
NO. 7.1
D ADEA13742 Standard; DNA; 63824 BP.
NO.2003.054143-A2.
PD 03-JUL-2003.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADN58769 standard; DNA; 20000 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR72312 standard; DNA; 63045 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAY-2004.
(ISIS-) ISIS PHARM INC.
(TAUP/) TAUPIER R J.
(GERL/) GERLACH V.
(GROS/) CROSSE W M.
(LIUX/) LIU X.
(ELLE/) ELLERWAN K.
(ROTH/) ROTHENBERG M.
(STON/) STONE D J.
(STON/) BURGESS C E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABOUT 1248

ID AD091189 stand**

PB Human cance

PD 22-

PA
                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2002.
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity
RESULT 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 1251
                                                                                                                                                                             Best Local Similarity
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Best Local Similarity
RESULT 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-SEP-2004.
(DOBI/) DOBIE K W.
(KOLL/) KOLLER E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human B7H DNA #4.
US2004102398-A1.
                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                 RESULT 1244
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US2003224380-A1.

PD 04-DEC-2003.
PD Best Local Similarity 82.6%; Pred. No. 1.6e-21;
PD Best Local Similarity 82.6%; Pred. No. 1.6e-21;
PD PACE6540 Etandard; DNA; 349901 BP.
DE Human GPCR gene SEQ ID NO:1393.
PN PRIZ70724-A2.
PN CA-DAN-2003.
PA (N-AD-) NAM-
PA (N-AD-) NAM-
                                                                                                                                                                                                                                                                                                                                                               PD 04-DEC-2003.

PA (GEHO) GEN HOSPITAL CORP.

Query Match
5.8%; Score 106.8; DB 12; Length 63824;
Best Local Similarity 8.6%; Pred. No. 7.9e-22;

RESULT 1254

DB ALG1326 standard; DNA; 91000 BP.

DE Human farnesoid X receptor (FXR) DNA #2.

PN W22003044167-A2.

PN WAZ-003.

PA (ISIS-) ISIS PHARM INC.

5.8%: Score 106.8; DB 9; Length 91000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.8%; Score 106.8; DB 11; Length 110000; 75.9%; Pred. No. 1.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 349901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 110000;
                                                               5.8%; Score 106.8; DB 10; Length 63824; 82.6%; Pred. No. 7.9e-22;
                                                                                                                                                                                                                                       Score 106.8; DB 12; Length 63824; Pred. No. 7.9e-22;
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DB Human ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 98546;
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(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

ery Match

1.8%; Score 106.8; DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 106.8; DB 11;
Pred. No. 1e-21;
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                                                                                                                                                                                                                                                                                                    ADH54221 standard; DNA; 63824 BP.
Human KNSL1 gene variant DNA sequence SeqID348.
US2003224380-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE43315 standard; DNA; 202100 BP.
Human IDE/ KNSL1 genomic sequence, SEQ ID 484.
WO2003054143-A2.
03-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABV50808 standard; cDNA; 426 BP.
Human prostate expression marker cDNA 50799.
                                                                                                                          ADH54220 standard; DNA; 63824 BP.

Human KNSL1 gene DNA sequence SeqID347.
US200324380-A1.
04-DEC-2003.
04-DEC-2003.
5.8%; Score 106.

ETY Match
st Local Similarity 82.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACN44790 standard; DNA; 98546 BP.
Human genomic sequence hCG23145.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO.C.C.
12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
HATCH ALCH 5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NEUR-) NEUROGENETICS INC. (GEHO ) GEN HOSPITAL CORP.
03-JUL-2003.
(NEUR-) NEUROGENETICS INC.
(GEHO ) GEN HOSPITAL CORP.
                                                          Query Match
Best Local Similarity
RESULT 1252
                                                                                                                                                                                                                                                         Best Local Similarity RESULT 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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RESULT 1256
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RESULT 1258
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ADR52994 standard; DNA; 128978 BP
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(BARA/) BARASH S C.
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADR07572 standard; cDNA; 4095 BP.
Full length human cDNA useful for treating neurological disease Seq 1078.
EP1447413-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK42366 standard; DNA; 1382 BP.
Genomic sequence #265 encoding novel human connective tissue polypeptide.
WO200155343-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK81284 standard; DNA; 442 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38096.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                              PD 10-MAR-2004.

PD 10-MAR-2004.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match

Best Local Similarity 78.0%; Pred. No. 1e-22;

RESULT 1265

ID AAH16642 standard; CDNA; 3112 BP.

DE Human CDNA sequence SEQ ID NO:1=7.

PN EP1074617-A2.

PD 07-PEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12; Length 48001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-AUG-2004.
(REAS-) RES ASSOC BIOTECHNOLOGY.
ery Match 5.8*; Score 106.6; DB 13; Length 4095;
                                                                                                                                                                                                                                                                                                                                                               Query Match 5.8%; Score 106.6; DB 4; Length 1754; Best Local Similarity 78.0%; Pred. No. 1e-22; RESULT 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 71.6%; Pred. No. 1.4e-22;
RESULT 1266
DE FULL length human CDNA, 4095 BP.
PD FAUGUST 1260
PD FULL length human CDNA useful for treating neurological disease PD ab. 40G-2004.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                   Query Match 5.8%; Score 106.6; DB 4; Length 553; Best Local Similarity 71.6%; Pred. No. 5e-23; RESULT 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.

TY Match

Local Similarity 70.1%; Pred. No. 5.1e-23;
                                                            Length 426;
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.8%; Score 106.6; DB 5;
Best Local Similarity 76.8%; Pred. No. 4.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.8%; Score 106.6; DB 8;
80.0%; Pred. No. 1.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.8%; Score 106.6; DB 1 75.3%; Pred. No. 7.7e-22;
                                                                                                    Human cDNA clone (3'-primer) SEQ ID NO:10067. BP1074617-A2.
                                                                                                                                                                                                                                                                                  AAK94142 standard; cDNA; 1754 BP.
Human full-length cDNA, SEQ ID NO: 2652.
EP1130094-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACA64961 standard; DNA; 152141 BP.
Human BCR DNA corresponding to U07000.
DE10127572-A1.
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                                                                                                                                                                                                                                                                                                                                             05-SEP-2001.
(HELI-) HELIX RES INST.
                                                                                                                                                                                    07-FEB-2001.
(HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC.
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Best Local Similarity
RESULT 1270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1268
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AAF97846 standard; DNA; 51474 BP.
Human neuroblastoma cell line NB-1 1p36 nucleotide seguence SEQ ID NO:60.
WO200116311-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAS27687 standard; DNA; 24757 BP.
DNA encoding novel.signal transduction pathway protein, Seq ID 1347.
WO200154733-A1.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Match 5.8%; Score 106.4; DB 8; Length 128978; Local Similarity 81.7%; Pred. No. 1.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.8%; Score 106.4; DB 10; Length 24757;
83.0%; Pred. No. 6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 128978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Length 24757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 51474;
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 106.4; DB 4; Length 1382;
Best Local Similarity 79.6%; Pred. No. 1e-22;
                                                                                                                                                                   20-MAR-2003.
(HUMA-) HUMAN GENOME SCI INC.
Sry Match 5.8%; Score 106.4; DB 9; Length 1382;
st Local Similarity 79.6%; Pred. No. 1e-22;
                                                                                                                                                                                                                                                                                                                                                                         Match 5.8*; Score 106.4; DB 12; Length 2419; Local Similarity 79.3*; Pred. No. 1.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK83459 standard; cDNA; 128978 BP.
Human cDNA differentially expressed in granulocytic cells #30
WO200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding human secreted protein, Seq ID No 764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.8%; Score 106.4; DB 6; Best Local Similarity 81.7%; Pred. No. 1.6e-21; RESULT 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD 08-MAR-2001.
PA (HISM) HISMAITSU PHARM CO LTD.
PA (CHISM) CHIBA PREFECTURE.
Cuery Match
Best Local Similarity 83.5%; Pred. No. 9.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.8%; Score 106.4; DB 83.0%; Pred. No. 6e-22;
                                                                                                AAD54587 standard, DNA; 128978 BP.
Human LIM kinase (LIMK) DNA #6.
WO200299048-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB94490 standard; DNA; 24757 BP.
Novel human protein DNA #99.
US2002168711-A1.
                                                                                                                                                                                                                                                                  AD064085 standard; cDNA; 2419 BP.
Novel human cDNA sequence #1246.
EP1440981-A2.
                                                                                                                                                                                                                                                                                                                             28-JUL-2004.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-APR-2002.
(GENE-) GENE LOGIC, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-DEC-2002. (EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
RESULT 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
SULT 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
RESULT 1276
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Length 32190;

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ADJ08821 standard; DNA; 32190 BP.
Human cardiovascular system associated polypeptide-related DNA SeqID2209.
US2004005575-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33087
WO200157182-A2.
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(SAGR-) SAGRES DISCOVERY INC.
5.8%; Score 106.2; DB 13; Length 122656;
                                                                                                                                                                                                                                                                                       PD 27-WAR-2003.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 5.8%; Score 106.2; DB 10; Length 32190;
Best Local Similarity 75.6%; Pred. No. 8.1e-22;
RESULT 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 106.2; DB 11; Length 39148; Pred. No. 9.1e-22;
Query Match 5.8%; Score 106.2; DB 12; Length 26865;
Best Local Similarity 78.6%; Pred. No. 7.3e-22;
RESULT 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.8%; Score 106.2; DB 12; Length 73063; 78.6%; Pred. No. 1.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%; Score 106.2; DB 4; Length 35959; 78.6%; Pred. No. 8.7e-22;
                                                                                Human cardiovascular system antigen genomic DNA SEQ ID No 2209.
WO200155321-A2.
02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                          ADE47403 standard; DNA; 32190 BP.
Human cardiovascular system related genomic DNA #969.
US2003059908-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                GB-JAN-2004.

(HUMA-) HUMAN GENOME SCI INC.

5.8%; Score 106.2; DB 13;

ery Match

75.6%; Pred. No. 8.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is-JUL-2004.

(SAGR-) SAGRES DISCOVERY INC.

Query Match

Section 13;

Best Local Similarity 74.2%; Pred. No. 9.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADQ97727 standard; DNA; 73063 BP.
Human cancer associated sequence HD10-034, SBQ ID
W02004060304-A2.
22-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PA (RAPP/) RAPPOLD-HOERBRAND G.
Query Match
5.8%; Score 106.2; DB 3;
Best Local Similarity 78.6%; Pred. No. 9.2e-22;
RESULT 1294
                                                                                                                                                               5.8%; Score 106.2; DB 4; 75.6%; Pred. No. 8.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC61681 standard; DNA; 39796 BP.
Nucleotide sequence of the human ataxia gene.
WO200058461-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABD33414 standard; DNA; 39983 BP.
Human cancer-associated (CA) gene HD07-077.
WO2004058146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABD33616 standard; DNA; 122656 BP.
Human cancer-associated (CA) gene HD07-125.
WO2004058146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACN43878 standard; DNA; 39148 BP.
Human genomic sequence hCG36720.
WO2003073826-A2.
                                                           AAS36709 standard; DNA; 32190 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1291
ID AAK78275 standard; DNA; 35959 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%;
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                                                                                                                                                                                Best Local Similarity
RESULT 1289
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RESULT 1293
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RESULT 1296
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                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24043 WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB83225 standard, cDNA, 688 BP.
Human cDNA sequence useful for the treatment of cancer (SeqID 1438)
WO2003050236-A2.
                                                                                                                                                                   DB 13; Length 128978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SAGR.) SAGRES DISCOVERY INC.
Query Match 5.8%; Score 106.4; DB 13; Length 243390;
Best Local Similarity 71.1%; Pred. No. 2.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 167932;
                                                                                                                                                                                                                                                                                                                                  5.8%; Score 106.4; DB 6; Length 163350; 77.7%; Pred. No. 1.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACC46358 standard; cDNA; 3084 BP.
Human dithp zinc finger transcriptional regulator-encoding cDNA
WO200297031-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACC46314 standard; cDNA; 3077 BP.
Human dithp zinc finger transcriptional regulator-encoding cDNA
WO200297031-A2.
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Prostate and breast cancer associated human gene CYP17.
W02004028346-A2.
08-ARR-2004.
(AMSH ) AMERSHAM BIOSCIENCES SV CORP.
                                                                                                                                                                                                                                                                                                                                                                                         ADL11501 standard; DNA; 167932 BP. Osteoarthritis-associated polymorphic nucleotide #33 WO2003054166-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUL-2003.
(INCY-) INCYTE GENOMICS INC.
6ry Match 5.8%; Score 106.4; DB 10;
6ry Match 79.3%; Pred. No. 1.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.8%; Score 106.2; DB 8; Best Local Similarity 74.2%; Pred. No. 1.9e-22; RESULT 1285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.8%; Score 106.2; DB 9; 82.2%; Pred. No. 7.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8;
                                                                                                                                                               5.8%; Score 106.4; DB 13
81.7%; Pred. No. 1.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 74.2%; Score 106.2; DB 8
Best Local Similarity 74.2%; Pred. No. 1.9e-22;
ID AAK69231 standard; DNA; 8658 BP.
DB Human immune/haematopoietic antigen genomic sequence by 09-2015/182-A2.
PD 09-2015/182-A2.
PD 09-2016-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%; Score 106.2; DB 4 78.6%; Pred. No. 3.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABD33366 standard; DNA; 243390 BP.
Human cancer-associated (CA) gene HD07-067.
WQ2004058146-A2.
15-JUL-2004.
  Drug therapy altered expressed gene #345.
WO2004072265-A2.
26-AUG-2004.
                                                                                                                                                                                                                              AAD46127 standard; DNA; 163350 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                 Human tumour suppressor gene. WO200268468-A2.
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                                                                                                                    (DORN/) DORNER A J. (TREP/) TREPICCHIO W L.
                                                                                                                                                                                                                                                                                                                                                                                                                       J6-A2.

...Y-) INCYTE GENON

LOCAL SIMILARITY 7

RESULT 1282

ID ABD33366 standa-
DE Human cance-
PN WO20040-
PD 15-
PA
                                                           (AMHP ) WYETH.
(BURC/) BURCZYNSKI M.
(TWIN/) TWINE N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                       06-SEP-2002.
(PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-DEC-2002
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                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                           BBBBB
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Length 32190

Length 39983;

704

Length 39796;

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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22051.
                                                                                                                                                                                                                                                                                                   Human musculoskeletal system-associated genomic DNA - SEQ ID 2322.
US2004009488-A1.
                                                                    ABXS8945 standard; cDNA; 16106 BP.
cDNA encoding novel human musculoskeletal system antigen #1289.
US2002147140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK83573 standard; cDNA; 130263 BP.
Human cDNA differentially expressed in granulocytic cells #144.
WO200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-APR-2002.
(GENE-) GENE LOGIC INC.
ery Match 5.8%; Score 106; DB 6; Length 130263;
        Score 106; DB 4; Length 16106;
Pred. No. 6.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADS36492 standard; DNA, 34059 BP.
Human autoimmune disease-related genomic DNA sequence
WO2004083403-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADS36465 standard; DNA; 25322 BP.
Human autoimmune disease-related genomic DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.8%; Score 106; DB 13; 79.6%; Pred. No. 9.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 106; DB 12;
Pred. No. 1.5e-21;
                                                                                                                                                                                                                                                                                                                                             PD 15-JAN-2004.

PA (HUMA-) HUMAN GENOME SCI INC.

QUERY MATCh 5.8*; Score 106; DB 12;

Best Local Similarity 79.6*; Pred. No. 6.2e-22;

RESULT 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%; Score 106; DB 13; 79.6%; Pred. No. 8.1e-22;
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Pred. No. 1.8e-21;
                                                                                                                                                                                                                  5.8%; Score 106; DB 8; 79.6%; Pred. No. 6.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
5.8%; Score 106; DB 4;
Best Local Similarity 77.9%; Pred. No. 9.1e-22;
RESULT 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%; Score 106; DB 8; 73.7%; Pred. No. 1.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ53477 standard; DNA; 70000 BP. Human PPP3CB genomic DNA #3. US2004023382-A1.
                                                                                                                                                                                                                                                                                  DNA; 16106 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABQ77243 standard; DNA; 57130 BP.
Human MARK DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA; 30393 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACH01384 standard; DNA; 96898 BP.
        5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WOLOCY-2003.
30-OCT-2003.
(UVSF-) UNIV SOUTH FLORIDA.
GETY MATCh. -... 5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-FEB-2004.

( (ISIS-) ISIS PHARM INC.
Ouery Match
Best Local Similarity 77.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004083403-A2.
30-SEP-2004.
(APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-SEP-2004.
(APPL-) APPLERA CORP.
                          Best Local Similarity RESULT 1305
                                                                                                                                                   (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                              Query Match
Best Local Similarity
SULT 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local_Similarity
RESULT 1308
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RESULT 1310
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK67239 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 1311
                                                                                                                                                                                                                                                                             ADJ29695 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human BIVM gene.
WO2003089595-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB99093 standard; cDNA; 4421 BP.
Human retinal pigment epithelial-derived factor (PEDF) genomic DNA #3.
US20031096750-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK67366 standard; DNA; 16106 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL35957 standard; DNA; 16106 BP.
Human musculoskeletal system related polynucleotide SEQ ID NO 2322.
WO200155367-A1.
                                                                                                                                                   5.8%; Score 106.2; DB 12; Length 137000; 70.9%; Pred. No. 2e-21;
                                                                                                                                                                                                                                                                                                                       5.8%; Score 106.2; DB 13; Length 161531; 78.6%; Pred. No. 2.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 349901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 16106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABS57269 standard; DNA; 4421 BP.
Partial sequence #3 of genomic DNA encoding human PEDF. US6451763-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

FY MAtch

L Local Similarity 78.6%; Pred. No. 3.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 106; DB 10;
Pred. No. 2.8e-22;
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      70.9%; Pred. No. 1.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.8%; Score 106; DB 9; 77.6%; Pred. No. 7.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.8%; Score 106; DB 4; 79.6%; Pred. No. 6.2e-22;
                                                                                                                                                                                                              ABD33232 standard; DNA; 161531 BP.
Human cancer-associated (CA) gene HD07-038.
WO2004058146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-SEP-2002.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                              ADC86940 standard; DNA; 349901 BP.
Human GPCR gene SEQ ID NO:1393.
EP1270724-A2.
                                           ADH77370 standard; DNA; 137000 BP.
Human PTPN12 polynucleotide #1.
US2003232434-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACH39496 standard; cDNA; 562 BP.
Human foetal brain cDNA #863.
US2003073623-A1.
                                                                                                                                                                                                                                                                           15-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DRWA)) DRWANAC R T.
(LABA)) LABAT I.
(STAC/) STACHE-CRAIN B.
(DICK/) DICKSON M C.
(JONE/) JONES L W.
                                                                                                                               (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOMB/) TOMBRAN-TINK J.
Best Local Similarity
RESULT 1297
ID ADH77370 standard; DN DE Human PTPN12 polynucl PN US2003232444-Al.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (STEE/) STEELE F R. (CHAD/) CHADER G J. (BECE) BECERRA S P. (JOHN/) JOHNSON L V. (RODR/) RODRIGUEZ I R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 1304
ID AAL35957 standard; DN
DE Human musculoskeletal
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME
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Best Local Similarity
RESULT 1302
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                                                                                                                                                Query Match
Best Local Similarity
RESULT 1298
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Best Local Similarity
RESULT 1299
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RESULT 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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- SEQ ID 1706.

Length 30393;

Length 34059

Length 57130;

Length 96898;

Length 70000;

PPREE

- SEQ ID 1679

Length 16106,

Length 16106;

Length 25322;

Query

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10-JUN-2004.

(ISIS-) ISIS PHARM INC.

5.7%; Score 105.8; DB 12; Length 19300;

Cuery Match

5.7%; Pred. No. 8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 105.8; DB 11; Length 99886; Pred. No. 2.2e-21;
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ry Match
5.7%; Score 105.8; DB 11; Length 31397;
t Local Similarity 78.9%; Pred. No. 1.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK84639 standard; cDNA; 9457 BP.
Human cDNA differentially expressed in granulocytic cells #1210.
WO200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%; Score 105.8; DB 5; Length 2823; 77.6%; Pred. No. 2.5e-22;
                                                                                                                          Length 218336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9457;
                 ABQ76678 standard; DNA; 218336 BP.
Androgen receptor signalling pathway-associated DNA AF067844.
WQ200282081-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2569;
                                                                                                                                                                                                                                                                                                           Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABA20423 standard; DNA; 2569 BP.
Human nervous system related polynucleotide SEQ ID NO 12754.
WO200159063-A2.
                                                                                                                                                                                                                                                                                                           5.7%; Score 105.8; DB 6; 80.6%; Pred. No. 8.9e-23;
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(GENE-) GENE LOGIC INC.

sry Match

5.7%; Score 105.8; DB 6;

rry Match

78.9%; Pred. No. 5.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMAN GENOME SCI INC.

17%; Score 105.8; DB 5;

12 Local Similarity 82.9%; Pred. No. 2.3e-22;
                                                                                                                                                                              ABN60296 standard; cDNA; 529 BP.

Human cancer related polynucleotide SEQ ID NO 263
W0200214500-A2.
21-FEB-2002.
(CHIR ) CHIRON CORP.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-2001.
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
ery Match
5.7%; Score 105.8; DB 5;
ery match
70.9%; Pred. No. 9.4e-23;
                                                                                                                  Query Match
Best Local Similarity 76.4%; Pred. No. 3e-21;
RESULT 1315
DE Human cancer related polynucleotide SEQ ID NO 26
PN W020014500-A2.
PD A (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adie5097 standard; cDNA; 2823 BP.

Human zinc finger protein 15 coding sequence.
W0200188690-A1.

(SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP74371 standard; DNA; 19300 BP.
Human X chromosome nucleotides 469701-489000.
US2004110156-A1.
                                                                                                                                                                                                                                                                                                                                                                                           Human prostate expression marker cDNA 54120.
WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1322
ID ACN44066 standard; DNA; 99886 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACN44346 standard; DNA; 31397 BP.
Human genomic sequence hCG33404.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                      ABV54129 standard; cDNA; 585 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genomic sequence hCG15674. WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 80.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-2003. (SAGR-) SAGRES DISCOVERY.
                                                                             17-OCT-2002.
(UYRP ) UNIV ROCHESTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001.
2001.
2001.
2ry Match
Best Local Similarity 7.
RESULT 1319
ID ABK84639 standa
DE Human CDNA
PD 11.
PA
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Best Local Similarity
RESULT 1318
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RESULT 1321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 1317
                                                                                                                                                                                                                                                                                                                          Best Local Similarity
RESULT 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-2003
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                                                                                                                                                                                                                                                                                                              Query Match
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RESULT 1314
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PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.

Query Match
5.7%; Score 105.8; DB 11; Length 133632;
Best Local Similarity 82.5%; Pred. No. 2.6e-21;
RESULT 1326
ID AD019501 standard; DNA; 135005 BP.
DE Human soft Lissue sarcoma-upregulated DNA - SEQ ID 2320.
PN WO20040408938-A2.
PD 10-JUN-2004
PA (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vuery Match 5.7%; Score 105.8; DB 12; Length 135005; Best Local Similarity 75.8%; Pred. No. 2.6e-21; RESULT 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.7%; Score 105.8; DB 13; Length 136284; Best Local Similarity 82.5%; Pred. No. 2.6e-21;
                                                                                                                                      Length 101685;
                                                                                                                                                                                                           Length 110000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-AFK-2002.
(GGNE-) GENE LOGIC INC.
iry Match
ir Local Similarity 82.5%; Pred. No. 2.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK83575 standard; cDNA; 136284 BP.
Human cDNA differentially expressed in granulocytic cells #146.
WO200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1329

ID AAL20897 standard; CDNA; 430 BP.

ID B Human breast cancer expressed polynucleotide 13354.

PN W0200151628-A2.

PD 19-JUL-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

SOLEY MATCH

5.7%; Score 105.6; DB 4; Length 430;

Best Local Similarity 72.6%; Pred. No. 9.1e-23;

RESULT 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7%; Score 105.6; DB 3; Length 438; 68.6%; Pred. No. 9.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 531;
                   ADQ17329 standard; DNA; 101685 BP.
Human soft tissue sarcoma-upregulated DNA - SEQ ID 146.
WO2004048938-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABN65723 standard; cDNA; 531 BP.
Human cancer related polynucleotide SEQ ID NO 5690.
WO200214500-A2.
                                                                           PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match

Best Local Similarity 73.2%; Pred. No. 2.2e-21;

RESULT 1324
                                                                                                                                                                                                           5.7%; Score 105.8; DB 10; 77.3%; Pred. No. 2.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.7%; Score 105.6; DB 6; 78.2%; Pred. No. 1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC27700 standard; cDNA; 438 BP.
Human secreted protein 5' EST, SEQ ID NO: 31775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR52798 standard; DNA; 136284 BP.
Drug therapy altered expressed gene #149.
WO2004072265-A2.
                                                                                                                                                                                                                                                            Lucar scandard; DNA; 133632 BP. Human genomic sequence hCG28560. WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DORN/) DORNER A J. (TREP/) TREPICCHIO W L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-AUG-2004.
(AMHP ) WYETH.
(BURC/) BURCZYNSKI M.
(TWIN/) TWINE N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2002.
(CHIR ) CHIRON CORP.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
RESULT 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1332
                                                                                                                                                                                                                            Best Local Similarity RESULT 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1033401-A2.
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                                                                                                                                                                                                                Query Match
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RESULT 1323
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PAPORE

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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40806 WO200157182-A2.
                                                                                                                                                                                 Best Local Similar...,
RESULT 1342
ID ADJ30876 standard, DNA, 6558 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3503.
PN US2004009488-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 105.6; DB 11; Length 175077; Pred. No. 3.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.7%; Score 105.6; DB 12; Length 139389; 75.2%; Pred. No. 3.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.7%; Score 105.6; DB 11; Length 122923; Best Local Similarity' 77.9%; Pred. No. 2.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 75.2%; Pred. No. 3.1e-21;
RESULT 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9; Length 139389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK84795 standard; cDNa; 139389 BP.
Human cDNA differentially expressed in granulocytic cells #1366.
WO200228999-A2.
                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
ry Match
t Local Similarity 81.7%; Pred. No. 4.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMAN GENOME SCI INC.
ry Match
t Local Similarity 78.2%; Pred. No. 1.8e-21;
ABX60126 standard; cDNA; 6558 BP.
cDNA encoding novel human musculoskeletal system antigen #2470.
US2002147140-A1.
                                                                                                                                                             5.7%; Score 105.6; DB 8; Length 6558; 81.7%; Pred. No. 4.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ7148 standard; cDNA; 139389 BP.
Human malignant pleural mesothelioma (MPM) cDNA #27.
US2003219760-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISIS-) ISIS PHARM INC.

ry Match S.7%; Score 105.6; DB 6;

t Local Similarity 71.5%; Pred. No. 1.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.7%; Score 105.6; DB 9. Best Local Similarity 75.2%; Pred. No. 3.1e-21; RESULT 1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BGHM ) BRIGHAM & WOMENS HOSPITAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB70369 standard; cDNA; 139389 BP.
PAC 6802 cDNA SEQ ID NO:61.
WO2003021229-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACN44026 standard; DNA; 122923 BP.
Human genomic sequence hCG24510.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACN44626 standard; DNA; 175077 BP.
Human genomic sequence hCG19724.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABS67634 standard; DNA; 63000 BP.
Human casein kinase-2 genomic DNA,
WO200262818-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                 AAK85994 standard; DNA; 59060 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wolver
12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
For Match - '-1arity 78.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
RESULT 1344
                                                                       10-OCT-2002.
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 1343
                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * Best Local Similarity RESULT 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
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Best Local'S:
RESULT 1345
                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                    AAK66534 standard; DNA; 1448 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21346.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI97535 standard, DNA, 5989 BP.
Human respiratory system associated polypeptide-related DNA SeqID999.
US2003077704-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK86101 standard; DNA; 6558 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40913.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS28565 standard; DNA; 5989 BP.
Genomic sequence #405 encoding for novel human respiratory antigen.
WO200155448-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL37138 standard; DNA; 6558 BP.
Human musculoskeletal system related polynucleotide SEQ ID NO 3503.
WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.7%; Score 105.6; DB 11; Length 5989;
Best Local Similarity 78.2%; Pred. No. 4.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
ry Match
t Local Similarity 78.2%; Pred. No. 4.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 3977;
                                                                                                                                                                                                                                                                    09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
5.7%; Score 105.6; DB 4; Length 1448;
-- 7.0.1 Similarity 69.4%; Pred. No. 1.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.7%; Score 105.6; DB 4; Length 6558;
Best Local Similarity 81.7%; Pred. No. 4.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 5.7%; Score 105.6; DB 5; Length 6558; Best Local Similarity 81.7%; Pred: No. 4.8e-22; RESULT 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%; Score 105.6; DB 4; Length 5989; 78.2%; Pred. No. 4.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 6558;
                                                                                                                                        Length 658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABĀZIJ72 standard; DNA; 6558 BP.
Human nervous system related polynucleotide SEQ ID NO 13703.
WO200159063-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human respiratory system associated genomic DNA seg id 999. US2003215893-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Lear Match Best Local Similarity 81.7%; Score 105.6; DB 4; 1 Best Local Similarity 81.7%; Pred. No. 4.8e-22; ID ABA21372 standard; DNA; 6558 BP. DE Human nervous system related by WO200159063-A2. PD H-6-AUG-2007.
                     Human cancer related polynucleotide SEQ ID NO 2511. WO200214500-A2.
                                                                                                                                     5.7%; Score 105.6; DB 6; 79.9%; Pred. No. 1.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%; Score 105.6; DB 1
81.7%; Pred. No. 3.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                         ADQ63489 standard; cDNA; 3977 BP.
Novel human cDNA sequence #650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REAS-) RES ASSOC BIOTECHNOLOGY.
  ABN62544 standard; cDNA; 658 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADG41761 standard; DNA; 5989 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                        LA2.

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2001.

LAZ.

LOA. HUMAN GENOME

LETY MATCH

BEST LOCAL Similarity 6.

RESULT 1334

ID AD063489 standar

PD AD063489 STANDAR
                                                                                        (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 1337
                                                                                                                                                         Best Local Similarity RESULT 1333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 1336
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Length 63000;

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Query Match
Best Local Similarity
RESULT 1367
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RESULT 1363
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                                                                                                                                                                     Best Local Similarity RESULT 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-2003.
(SUGE-) SUGEN INC.
                                                                                                                                                                                                              ABT10875 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 79.2%; Pred. No. 3.5e-22;
RESULT 1356
DE Full length human cDNA, 3825 BP.
PP. EP1447413-A2.
                                                 PD 22-JUL-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
Querry Match
5.7%; Score 105.6; DB 12; Length 176771;
Best Local Similarity 78.2%; Pred. No. 3.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 76.7%; Score 105.6; DB 11; Length 344548;
RESULT 1354
                                                                                                                                                                                                                                                                       5.7%; Score 105.6; DB 10; Length 190000; 78.2%; Pred. No. 3.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                          5.7%; Score 105.6; DB 13; Length 227246; 76.7%; Pred. No. 4.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA34969 standard; DNA; 6210 BP.
Human adenosine receptor related polynucleotide SEQ ID NO:2658.
WO200009525-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7%; Score 105.4; DB 13; Length 3825; 79.2%; Pred. No. 4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-FEB-2000.
(UYEC-) UNIV EAST CAROLINA.
5.7%; Score 105.4; DB 3; Length 6210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.7%; Score 105.4; DB 2; Length 6210; Best Local Similarity 79.2%; Pred. No. 5.4e-22; RESULT 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1194396 standard; cDNA; 822 BP.
A1194396 standard; cDNA; 822 BP.
Human neuroblastoma expressed polynucleotide SEQ ID NO 471.
NO201066719-A1.
13-SEP-2001.
(CHIB-) CHIBA PREFECTURE.
(HISM ) HISAMITSU PHARM CO LTD.
ETY Match
ETY Match
ETY Match
ETY Match
ETY Match
ETY Match
ETY No. 1.66-22;
RESULT 1350
ID ADQ97167 standard; DNA; 176771 BP.
DE Human cancer associated sequence HD2-08-009, SEQ ID 143.
PN WO2004060304-A2.
                                                                                                                                                                                          Osteoarthritis-associated polymorphic nucleotide #284, WO2003054166-A2, 03-JUL-2003. (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                        ABD33372 standard; DNA; 227246 BP.
Human cancer-associated (CA) gene HD07-047.
WO2004058146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACN44070 standard; DNA; 344548 BP.
Human genomic sequence hCG36954.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADAS2859 standard; cDNA; 3098 BP.
Human coding sequence, SEQ ID 427.
EP1293569-A2.
                                                                                                                                                                          ADL13752 standard; DNA; 190000 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-AUG-2004.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ63815 standard; cDNA; 6210 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                .-a.
..cy-) INCYTE GENOM.
..ery Match
Best Local Similarity 72
RESULT 1352
ID ABD33272 standa-'
DE Human cance-
PW WO20040-'
PD 15-'
PA
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Best Local Similarity
RESULT 1353
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EP599077-A2.
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Human low adenosine antisense oligonucleotide related sequence #2658. W020062736-A2. 26-OCT-2000. (UYEC-) UNIV BAST CAROLINA. (NYCE-) NYCE J W.
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DE Human pulmonary and inflammatory target DNA #245.

PN W0200253309-A2.

PD 31-0CT-2002.

PA (EPIG-) EPIGENESIS PHARM INC.

Query Match

BEST Local Similarity 79.2%; Pred. No. 5.4e-22;

RESULT 1365

ID ADH17136 standard; CDNA; 6210 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vuery Match 5.7%; Score 105.4; DB 10; Length 6210; Best Local Similarity 79.2%; Pred. No. 5.4e-22; RESULT 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7%; Score 105.4; DB 10; Length 6210; 79.2%; Pred. No. 5.4e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6210;
                                                                                                                                                                                                                                                                                                         Human breast cancer associated coding sequence SEQ ID NO: 1009 WO200259271-A2.
                                                                                                                                                                                                                                                                                                                                                           PD 01-AUG-2002.

PA (GENE-) GENE LOGIC INC.

Query Match 5.7%; Score 105.4; DB 6; Length 6210;

Best Local Similarity 79.2%; Pred. No. 5.4e-22;

RESULT 1361
                                                                                                                                                                                                       Length 6210;
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Renal cell carcinoma differentially expressed gene #141.
WO2004048933-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABZ35089 standard; cDNA; 6210 BP.
Human gene expression profile polynucleotide SEQ ID NO WO200274979-A2.
26-SEP-2002.
(ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACC46752 standard; cDNA; 6210 BP.
Human COPD related protein encoding cDNA SEQ ID NO:3.
WO200297127-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%; Score 105.4; DB 12; 79.2%; Pred. No. 5.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.7%; Score 105.4; DB 6; 79.2%; Pred. No. 5.4e-22;
                                                                                                                                                                                                       5.7%; Score 105.4; DB 3; 79.2%; Pred. No. 5.4e-22;
Best Local Similarity 79.2%; Pred. No. 5.4e-22; RESULT 1359
ID AAF21091 standard; DNA; 6210 BP.
                                                                                                                                                                                                                                                                                    CDNA; 6210 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABZ96785 standard; DNA; 6210 BP.
Human nucleic acid sequence.
WO200285308-A2.
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WO2003097854-A2.
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(EPIG-) EPIGENESIS PHARM INC.
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(BURC/) BURCZYNSKI M E
(TREP/) TREPICCHIO W L.
(DORN/) DORNER A.
(STOV/) SLOVER J A.
(SLON/) SLONI D K.
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23-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:84.
WO200116311-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF97871 standard; DNA; 23241 BP.
Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:85.
                                                                                                                                                                                                                                                                                                                                                            AAF21095 standard; DNA; 16595 BP.
Human low adenosine antisense oligonucleotide related sequence #2662.
WO20062736-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 16595;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 105.4; DB 11; Length 22477; Pred. No. 1.2e-21;
                                                                                                                                                                    Length 6210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.7%; Score 105.4; DB 3; Length 16595; 79.2%; Pred. No. 9.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 23241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 105.4; DB 5; Length 23241; Pred. No. 1.2e-21;
                                                                                                                                                                                                                       AAA34973 standard; DNA; 16595 BP.
Human adenosine receptor related polynucleotide SEQ ID NO:2662.
WO200009525-A2.
                                                                                                                                                                                                                                                                                                                           Score 105.4; DB 3; Length 16595; Pred. No. 9.8e-22;
                                                                                                                                                                    Score 105.4; DB 13;
Pred. No. 5.4e-22;
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Pred. No. 1.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 105.4; DB 5;
Pred. No. 1.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABD20638 standard; DNA; 16595 BP.
Human pulmonary and inflammatory target DNA #249.
WO200285309-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2002.
(EPIG-) EPIGENESIS PHARM INC.
(EPIG-) EPIGENESIS PHARM INC.
(EPY Match 5.7%; Score 105.4; DB 11
(EPIG-) Similarity 79.2%; Pred. No. 9.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-0CT-2002.
(EPIG-) EPIGENESIS PHARM INC.
Fry Match 5.7%; Score 105.4; DB 10
Fry Match 79.2%; Pred. No. 9.8e-22;
               Orug therapy altered expressed gene #188.402004072265-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA; 16595 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACN44910 standard; DNA; 22477 BP Human genomic sequence hCG22355.
ADR52837 standard; DNA; 6210 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HISM ) HISAMITSU PHARM CO LTD. (CHIB-) CHIBA PREFECTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HISM ) HISAMITSU PHARM CO LTD. (CHIB-) CHIBA PREFECTURE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABZ96789 standard; DNA; 1659
Human nucleic acid sequence
                                                                                                                                                                                                                                                                                 24-FEB-2000.
(UYEC-) UNIV EAST CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SAGR-) SAGRES DISCOVERY
                                                                                                                                                  TREPICCHIO W L.
                                                                       AMHP ) WYETH.
BURC/) BURCZYNSKI M.
TWIN/) TWINE N.
                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
RESULT 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                    Match
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                        Best Loca
RESULT 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1374
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12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
ery Match
ery Match 79.2%; Pred. No. 3.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 105.4; DB 10; Length 125515; Pred. No. 3.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 110000;
                                                                                                                                                                                                                                                                        (SAGRE) SAGRES DISCOVERY.

5.7%; Score 105.4; DB 11; Length 73967;

L Local Similarity 79.2%; Pred. No. 2.4e-21;
                                                                                  (INCY-) INCYTE GENOMICS INC.

ry Match
5.7%; Score 105.4; DB 10; Length 41369;
t Local Similarity 74.2%; Pred. No. 1.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 94752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH92222 standard; DNA; 700 BP.
Human inflammatory bowel disease related gene fragment IGR2234a.
WO200142511-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS42054 standard; DNA; 10085 BP.
Genomic sequence #370 encoding novel human enzyme polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL13941 standard; DNA; 125515 BP.
Osteoarthritis-associated polymorphic nucleotide #473.
                Osteoarthritis-associated polymorphic nucleotide #54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABN63732 standard; cDNA; 629 BP.
Human cancer related polynucleotide SEQ ID NO 3699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%; Score 105.4; DB 12; 79.2%; Pred. No. 3.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CELL-) CELLTECH R & D INC.
(UYRO-) UNIV ROTTERDAM BRASMUS.
TY MAtch 5.7%; Score 105.4; DB 10;
t Local Similarity 73.4%; Pred. No. 2.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 105.2; DB 6;
Pred. No. 1.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.7%; Score 105.2; DB 4; 76.9%; Pred. No. 1.6e-22;
                                                                                                                                                                                                                                                                                                                                                                    ADF11646 standard; DNA; 94752 BP.
Human chromosome 17 clone HPRC905N1 nucleic acid.
WO2003087763-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 105.2; DB 4 Pred. No. 1.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH10562 standard; cDNA; 574 BP.
Human cDNA clone (3'-primer) SEQ ID NO:7397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUN-2001.
.(WHED ) WHITEHEAD INST BIOMEDICAL RES.
(ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACN44026 standard; DNA; 122923 BP.
Human genomic sequence hCG24510.
WO2003073826-A2.
                                                                                                                                                                            ACN44438 standard, DNA, 73967 BP.
Human genomic sequence hCG27607.
WO2003073826-A2.
DNA; 41369 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS INC. ry Match 5.7%; t Local Similarity 77.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2001.
(HELI-) HELIX RES INST.
5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                              Best Local Similarity RESULT 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          local Similarity
                                         WO2003054166-A2.
03-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003054166-A2.
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Human genomic DNA encoding partial novel secreted protein, Seq ID 1698.
WO200155322-A2.
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Human genomic OCTN2 sequence.
WO200014210-A1.
                                                                                                                                       ABX74073 standard; DNA; 19472 BP. Human novel polynucleotide #901. US2002132753-A1.
                                         02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                 (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
RESULT 1401
                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RUBI/) RUBIN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 1402
                                                                                                                                                                                                   19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-AUG-200
                                                                                 Query Match
                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK73172 standard; DNA; 16555 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27984
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAK70102 standard; DNA; 16555 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24914
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAKI1070 standard; DNA; 17874 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25882.
WO200157182-A2.
                                                                                                                                                                                                                                                                         AAL17624 standard; DNA; 12452 BP.
Human musculoskeletal system related polynucleotide SEQ ID NO 3989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human musculoskeletal system-associated genomic DNA - SEQ ID 3989 US2004009488-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 12452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0--AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.7%; Score 105.2; DB 4; Length 17874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
5.7%; Score 105.2; DB 5; Length 12452;
cry Match
78.5%; Pred. No. 9.5e-22;
                                                                                                                                                                       03-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
5.7%; Score 105.2; DB 4; Length 10085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-4UG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
5.7%; Score 105.2; DB 4; Length 16555;
criferal Similarity 82.1%; Pred. No. 1.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMAN GENOME SCI INC.
ry Match
f. Local Similarity 82.1%; Pred. No. 1.1e-21;
                                                             Length 10085;
                                                                                                                                                                                                                                                                                                                                                                       5.7%; Score 105.2; DB 4; Length 12452; 78.5%; Pred. No. 9.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABX60612 standard; cDNA; 12452 BP.

cDNA encoding novel human musculoskeletal system antigen #2956.
10-0CT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7%; Score 105.2; DB 8; Length 12452; 78.5%; Pred. No. 9.5e-22;
   Query Match 5.7%; Score 105.2; DB 4; Length 1008. Best Local Similarity 80.2%; Pred. No. 8.4e-22; RESULT 1386. LOCAL Similarity 80.2%; Pred. No. 8.4e-22; DB 4. Length 1008. Best Local Similarity 80.2%; Pred. No. 8.4e-22; DB Human reproductive system related antigen DNA SEQ ID NO: 5491. PD 02-AUG-2001. PD (HUMA-) HIMAN ACCORD.
                                                                                                                                                                                                                                                                                                                                                                                                                               ABA21062 standard; DNA; 12452 BP.
Human nervous system related polynucleotide SEQ ID NO 13393.
WO200159063-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12;
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(HUMA-) HUMAN GENOME SCI INC.

6-ry Match

5.7%; Score 105.2; DB 1

5.7%; Pred. No. 9.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ31362 standard; DNA; 12452 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS26724 standard; DNA; 19472 BP
                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                               Best Local Similarity RESULT 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
RESULT 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
RESULT 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (RUBE/) RUBEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1393
                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1388
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Best Local Similarity
RESULT 1390
                                                                                                                                                                                                                                                                                                                 WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                 02-AUG-2001
                                                                                                                                                                                                                     Ouery Match
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AAS26966 standard; DNA; 25619 BP.
Human genomic DNA encoding partial novel secreted protein, Seq ID 302.
WO200155441-A2.
                                                                                                                                                                                                                                                                                                                          RESULT 1396

ID AAK73173 standard; DNA; 23885 BP.

ID B Human immunne/haematopoietic antigen genomic sequence SEQ ID NO:27985.

PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

5.7%; Score 105.2; DB 4; Length 23885;

Best Local Similarity 82.1%; Pred. No. 1.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK70103 standard; DNA; 23885 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24915.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAR-2000.
(CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
5.7%; Score 105.2; DB 3; Length 25871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.7%; Score 105.2; DB 4; Length 25619;
st Local Similarity 78.5%; Pred. No. 1.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.7%; Score 105.2; DB 6; Length 25619; 78.5%; Pred. No. 1.5e-21;
Match 5.7%; Score 105.2; DB 4; Length 19472; Local Similarity 74.1%; Pred. No. 1.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 25619;
                                                                                                                                                                                                                                                                          Length 19472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 23885;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6213
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Human reproductive system related antigen DNA SEQ ID NO:
W0200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
5.7%; Score 105.2; DB 5;
it Local Similarity 78.5%; Pred. No. 1.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match atch

Best Local Similarity 82.1%; Pred. No. 1.4e-21;

RESULT 1398
                                                                                                                                                                                                                                                                          5.7%; Score 105.2; DB 8; 74.1%; Pred. No. 1.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
5.7%; Score 105.2; DB 4;
Best Local Similarity 78.5%; Pred. No. 1.5e-21;
RESULT 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK72116 standard; DNA; 25619 BP.
Human ovarian antigen #15 genomic sequence #1.
WO200155329-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK91708 standard; DNA; 25619 BP.
Novel ovarian related polynucleotide #17.
US2002045230-A1.
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us-10-785-220b-11.rng.spdi

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Best Local Similarity RESULT 1414
                        YOUNG P E.
FERRIE A M.
                                                                                                                                              Best Local Similarity RESULT 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 1419
     GREENE J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADS89043 standard;
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                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001
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                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ12872 standard; DNA; 429 BP.
DNA fragment of a BAC clone that encodes a human secreted protein Seq726.
US2004010132-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADF13118 standard; DNA; 161652 BP.
Hypermethylation site in human breast cancer CpG island locus HBC-48.
US2003129602-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1411
ID AAK72510 standard; DNA; 429 BP.
DE Human immune/haematopoletic antigen genomic sequence SEQ ID NO:27322
PN WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.7%; Score 105.2; DB 12; Length 161652; 78.5%; Pred. No. 4.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 161652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 215221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 110000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 105.2; DB 10; Length 110000; Pred. No. 3.6e-21;
                                                                                                                                                                                                                                                                           5.7%; Score 105.2; DB 10; Length 47188; 69.5%; Pred. No. 2.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 54701;
                                                                                                                               DB 9; Length 26850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 429;
                                                                                                                                                                                  ADL13758 standard; DNA; 47188 BP.
Osteoarthritis-associated polymorphic nucleotide #290.
WO2003054166-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.7%; Score 105.2; DB 12; 78.5%; Pred. No. 4.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 105.2; DB 10;
Pred. No. 3.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WCAULTOON.

(BUMAL) HUMAN GENOME SCI INC.

(HUMAL) HUMAN GENOME SCI INC.

5.7%; Score 105; DB 4;

ery Match

79.5%; Pred. No. 1.4e-22;
                                                                                                                               5.7%; Score 105.2; DB 9 76.9%; Pred. No. 1.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 105.2; DB 1. Pred. No. 2.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 5.7%; Score 105.2; DB 1:
Best Local Similarity 82.1%; Pred. No. 5.4e-21;
   76.9%; Pred. No. 1.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AD137264 standard; DNA; 161652 BP.
Hypermethylation in cancer (HBC) locus-48.
US6605432-B1.
                                                                                                              (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
                                    ACF05020 standard; DNA; 26850 BP.
Human cation transporter OCTN2 gene.
WO2003054011-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACN44754 standard; DNA; 215221 BP.
Human genomic sequence hCG37990.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                               ACN44478 standard; DNA; 54701 BP.
Human genomic sequence hCG24071.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%;
                                                                                                                                                                                                                                                                                                                                                                            WOAVE-2003.
12-88-2003.
(SAGR-) SAGRES DISCOVERY.
GATY MATCH 5.7%;
                                                                                                                                                                                                                                     03-JUL-2003.
(INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RUBE/) RUBEN S M.
(FLOR/) FLORENCE K A.
                                                                                                                                              Best Local Similarity RESULT 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1410
Best Local Similarity RESULT 1403
                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 1405
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Best Local Similarity
RESULT 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROSEN C A.
BREWER L A.
DUAN R D.
RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUAN/) HUANG T H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-AUG-2003
                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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AAK82785 standard; DNA; 1276 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37597.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                     Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27117. W0200157182-A2.
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42341
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL98096 standard; DNA; 4026 BP.
Human testicular antigen encoding DNA fragment SEQ ID NO: 2748.
WQ200155317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 105; DB 13; Length 11001; Pred. No. 1e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AALO5213 standard; DNA; 4026 BP.
Human reproductive system related antigen DNA SEQ ID NO: 7901
WO200155320-A2.
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ry Match
5.7%; Score 105; DB 4; Length 13608;
t Local Similarity 77.8%; Pred. No. 1.2e-21;
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ry Match

t Local Similarity 73.4%; Pred. No. 5.5e-22;
                                                                                           Length 429;
                                                                                                                                                                                                                                                                               Length 1276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3252
                                                                                           5.7%; Score 105; DB 12; 79.5%; Pred. No. 1.4e-22;
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Pred. No. 9.8e-22;
                                                                                                                                                                                                                                                                          5.7%; Score 105; DB 4; 76.7%; Pred. No. 2.7e-22;
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ry Match
t Local Similarity 77.8%; Pred. No. 4.9e-22;
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Query Match
Best Local Similarity 73.4%; Pred. No. 5.5e-22;
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Human gene SEQ ID NO:130.
WO2004035803-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB54006 standard; DNA; 10224 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA; 10224 BP.
                                                                                                                                                                                                                                                                                                                                               AAK72305 standard; DNA; 3252 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human RASSF1 gene SEQ ID NO:59.
WO2004035803-A2.
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29-ART-2004.
(EPIC-) EPIGENOMICS AG.
*** Match '-'arity 76.3%;
                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
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PA (EPIG-) EPIGENOMICS AG.
QUEYY MATCh 5.7%;
Best Local Similarity 76.3%;
RESULT 1420
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WO2003072821-A2.
04-SEP-2003.
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(YUGG/) YU G.
(FLOR/) FLORENCE C.
(EBNE/) EBNER R.
(OLSE/) OLSEN H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 1415
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RESULT 1430
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Human thyroid tumour associated PKCG genomic sequence SEQ ID NO: 18.
WO200283727-A2.
                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2003.
(SAGR-) SAGRES DISCOVERY.
(ery Match 5.7%; Score 105; DB 10; Length 23328;
(ery Match 76.3%; Pred. No. 1.6e-21;
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Pred. No. 1.8e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.7%; Score 105; DB 10; Length 24801; 76.3%; Pred. No. 1.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 25301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%; Score 105; DB 12; Length 23328, 76.3%; Pred. No. 1.6e-21;
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                                                                                                                                                                                              Length 23328;
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Human RASSF1 carcinoma associated gene, SEQ ID NO:1442.
WO2003057146-A2.
RESULT 1421

ID ADA02918 standard; DNA; 23328 BP.

BE Human FUS1 carcinoma associated gene, SEQ ID NO:1436.

PN W02003057146-A2.

PD 17-JUL-2003.

PA (SAGR-) SAGRES DISCOVERY.

5 7%: Score 105; DB 9; Lengt
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Human protein kinase C gamma (PRKCG) genomic DNA.
US2004106138-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.7%; Score 105, DB 10;
Best Local Similarity 76.3%; Pred. No. 1.6e-21;
RESULT 1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADM74513 standard; DNA; 23328 BP.
Human carcinoma associated (CA) nucleic acid #91
US2004072154-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 105; DB 12;
Pred. No. 1.7e-21;
                                                                                                                                                                       Ouery Match Similarity 76.3%; Score 105; DB 9; Best Local Similarity 76.3%; Pred. No. 1.6e-21; RESULT 1422

DE AUMAN FUSI gene.

PN W02003008583-A2.

PD 30-7AN-2003.

PA (SAGR-) SAGRES DISCOVERY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA; 23328 BP.
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Best Local Similarity 76.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Fusl genomic sequence.
WO2003045230-A2.
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(SAGR-) SAGRES DISCOVERY.
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(SAGR-) SAGRES DISCOVERY.
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WO2003008583-A2.
30-JAN-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-2004.
(UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LANGE TO THE PAGE THE PAGE TO 
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(MORR/) MORRIS D W.
(ENGE/) ENGELHARD E K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRAPATORY

ACR/) MORRIS D W.

(ENGE/) ENGELHARD E

Best Local Similarity 7.

RESULT 1425

ID AB220990 stander

DE Human thyrr

PN WO20020**

PD 24**

PA
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2003.
2R-) SAGRES DISC.
2ry Match
Best Local Similarity ?
RESULT 1423
ID ADC85398 stand?
DE Human Fus!
PN WO2003'
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RESULT 1426
ID AD001541 standard; DN/
DE Human protein Kinase (
PN US2004106138-A1.
PD 03-UUN-2004.
PA (UNIW ) UNIV WASHINGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 1427
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Genomic sequence #428 encoding novel human connective tissue polypeptide. WO200155343-A1.
                                                                                                                                      5.7%; Score 105; DB 12; Length 27589; 76.3%; Pred. No. 1.8e-21;
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WO200155317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 70242;
                                                                                                                                                                                                                                                                                                                                                                                                         8220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AALÖ5631 standard; DNA; 32192 BP.
Human reproductive system related antigen DNA SEQ ID NO: 8319.
WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7945
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ID ADBG0685 standard; DNA; 32192 BP.

BD Connective tissue related genomic DNA #428.

PD Connective tissue related genomic DNA #428.

PD 20-MAR-2003.

PD 20-MAR-1 HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 73.6%; Pred. No. 2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AUG-2001.
(HUMA) HUMAN GENOME SCI INC.
127 Match 5.7%; Score 105; DB 4; Length 32192;
st Local Similarity 73.6%; Pred. No. 2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.7%; Score 105; DB 4; Length 32192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 5.7%; Score 105; DB 5; Length 32192; Local Similarity 73.6%; Pred. No. 2e-21;
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Human nervous system related polynucleotide SEQ ID NO 7659.
WQ200159063-A2.
                                                                                                                                                                                                                                                                                                                                                                                  AALO5532 standard; DNA; 32192 BP.
Human reproductive system related antigen DNA SEQ ID NO:
WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AALO5257 standard; DNA; 32192 BP.
Human reproductive system related antigen DNA SEQ ID NO:
WO200155320-A2.
ADM74519 standard; DNA; 27589 BP.
Human carcinoma associated (CA) nucleic acid #94
US2004072154-Al.
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(SAGR-) SAGRES DISCOVERY.
Query Match
Est Local Similarity, 77.8%; Pred. No. 3.2e-21;
                                                                                                                                                                                                                                                              02-AUG-2001.
(HDWA-) HUMAN GENOME SCI INC.
(HDWA-) HUMAN GENOME SCI INC.
5.7%; Score 105; DB 4;
ery Match 5.7%; Pred. No. 2e-21;
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ry Match

5.7%; Score 105; DB 4;

t Local Similarity 73.6%; Pred. No. 2e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genomic sequence hCG1784894 WO2003073826-A2.
                                                                                                                                                                                                       DNA; 32192 BP.
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(HUMA-) HUMAN GENOME SCI INC.
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                                                                   15-APR-2004.
(MORR/) MORRIS D W.
(ENGE/) ENGELHARD E K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 1435
                                                                                                                                    Query Match
Best Local Similarity
RESULT 1431
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RESULT 1434
                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity RESULT 1432
                                                                                                                                                                                                  ABK42529 standard;
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RESULT 1433
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14-NOV-2002
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                                                                                                                                                                                                                            07-FEB-200
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(SAGR-) SAGRES DISCOVERY INC.
ery Match 5.7%; Score 105; DB 12; Length 128963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 95914;
                                                                                                           Score 105; DB 11; Length 70242; Pred. No. 3.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 105; DB 10; Length 96589;
Pred. No. 3.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.7%; Score 105; DB 10; Length 96589;
Best Local Similarity 73.8%; Pred. No. 3.9e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA02954 standard; DNA; 96589 BP.
Human NR3C1 carcinoma associated gene, SEQ ID NO:1472.
WO2003057146-A2.
                                                                                                                                                                                                                                                                                                                                       Osteoarthritis-associated polymorphic nucleotide #11. WO2003054166-A2. 03-JUL-2003.
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                                                                                                                                                                ABL64158 standard; DNA; 84539 BP.
Stomach cancer related gene sequence SEQ ID NO:2495.
MVO20194629-A2.
13-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM74549 standard; DNA; 96589 BP.
Human carcinoma associated (CA) nucleic acid #109.
US2004072154-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ97110 standard; DNA; 128963 BP.
Human cancer associated sequence HD08-002, SEQ ID
WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 105; DB 12;
Pred. No. 3.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                       5.7%; Score 105; DB 10; 77.8%; Pred. No. 3.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.7%; Score 105; DB 13; 77.8%; Pred. No. 3.8e-21;
                                                                                                                                                                                                                                                                5.7%; Score 105; DB 6; 77.8%; Pred. No. 3.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 105; DB 9;
Pred. No. 3:9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABD33444 standard; DNA; 95914 BP.
Human cancer-associated (CA) gene HD07-084.
WO2004058146-A2.
             ACN44710 standard; DNA; 70242 BP.
Human genomic sequence hCG1784894
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                         ADL13479 standard; DNA; 84539 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB72692 standard; DNA; 96589 BP.
Human NR3C1 gene.
WO2003008583-A2.
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                                                             MC2VC--
12-SEC-2003.
(SAGR-) SAGRES DISCOVERY.
Hery Match 5.7%;
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5.7%;
Similarity 73.8%;
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Best Local Similarity 73.8%;
RESULT 1447
                                                                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Nr3cl genomic sequence WO2003045230-A2.
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(SAGR-) SAGRES DISCOVERY.
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                                                                                                                                                                                                                                              (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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Best Local Similarity
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Best Local Similarity
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RESULT 1439
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AAS27780 standard; DNA; 11336 BP.
DNA encoding novel signal transduction pathway protein, Seg ID 1440.
WO200154733-A1.
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Human sequence from clone RP5-1009E24 on chromosome 20 Contains DNA.
WO2003072827-A1.
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(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 5.7%; Score 104.8; DB 11; Length 57038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%; Score 104.8; DB 10; Length 11336; 82.4%; Pred. No. 1.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7%; Score 104.8; DB 12; Length 7136; 77.2%; Pred. No. 9.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 104.8; DB 13; Length 7136; Pred. No. 9.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.7%; Score 104.8; DB 12; Length 2988; 77.2%; Pred. No. 5.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Match 5.7%; Score 104.8; DB 13; Length 7136; Local Similarity' 77.2%; Pred. No. 9.1e-22;
                                                                                                                                Length 326002;
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                                                                                                                                                                                                                                                                                                                                          DB 4; Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADF83102 standard; cDNA; 7136 BP.
Human Pellino homologue 1 gene, overexpressed in cancer.
WO2003100000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human soft tissue sarcoma-upregulated DNA - SEQ ID 8135
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(BOANG-2001.

(HUMA-) HUMAN GENOME SCI INC.

5.7%; Score 104.8; DB 4;

ery Match

5.7%; Score 104.8; DB 4;
                                                                             PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.

QUERY MAtch

5.7%; Score 105; DB 13;

Best Local Similarity 81.3%; Pred. No. 8.1e-21;

RESULT 1449
                                                                                                                                                                                                                                                                                                        (HELL.) HELIX RES INST.

17 Match 5.7%; Score 104.8; DB 4

17 Local Similarity 78.8%; Pred. No. 1.9e-22;
ABD32843 standard; DNA; 326002 BP.
Human cancer-associated genomic DNA HD17-014.
WO2004074320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP24928 standard; cDNA; 7136 BP.
PRO polypeptide encoding cDNA SEQ ID NO:2106.
WO2004041170-A2.
                                                                                                                                                                                             AAH09669 etandard; cDNA; 552 BP.
Human cDNA clone (3'-primer) SEQ ID NO:6504.
EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP56419 standard; cDNA; 7136 BP.
Human PRO cDNA sequence SEQ ID NO:2395.
WO2004039956-A2.
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Novel human protein DNA #192.
US2002168711-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004048938-A2.
10-JUN-2004.
(PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                  ADQ25315 standard; DNA; 2988 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 5.7%;
Local Similarity 77.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAY-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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RESULT 1456
ID
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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Human macroprotein 10.01-encoding cDNA

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PD 22-JUL-2004.

PA (SAGR-) SAGRES DISCOVERY INC.

Querry Match

5.7%; Score 104.8; DB 12; Length 138627;

Best Local Similarity 79.1%; Pred. No. 5.6e-21;

RESULT 1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11; Length 181684;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 104.8; DB 13; Length 110000; Pred. No. 4.9e-21;
                                                                                                                                                                                                                                                                                                                                                    Length 106378;
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                                                                                                                                                                                                         DB 11; Length 92794;
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PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
BEST Local Similarity 78.1%; Pred. No. 3.68-22;
ID ABO77944 Attach
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Query Match 5.7%; Score 104.6; DB 4; Length 387;
Best Local Similarity 72.2%; Pred. No. 1.8e-22;
                                                                                                           ADP65471 standard; DNA; 92794 BP.
Human sequence from clone RP5-1009E24 on chromosome 20 DNA.
WO2003072827-A1.
04-SEP-2003.
(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ97183 standard; DNA; 138627 BP.
Human cancer associated sequence HD08-011, SEQ ID 159.
WO2004060304-A2.
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29-MAY-2003.

(MILL-) MILLENNIUM PHARM INC.

6ry Match 5.7%; Score 104.6; DB 11;

6ry Match 72.2%; Pred. No. 3e-22;
                                                                                                                                                                                                                                                                                                                                                  Score 104.8; DB 11;
Pred. No. 4.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL12012 standard; cDNA; 387 BP.
Human breast cancer expressed polynucleotide 4469.
WO200151628-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.7%; Score 104.8; DB 11 Best Local Similarity 78.8%; Pred. No. 6.6e-21; RESULT 1463
                                                                                                                                                                                                          5.7%; Score 104.8; DB 11
80.5%; Pred. No. 4.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 104.8; DB 13
Pred. No. 4.9e-21;
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                                                                                80.5%; Pred. No. 3.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Breast cancer related marker, seq id 3350. US2003099974-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACN44374 standard; DNA; 181684 BP.
Human genomic sequence hCG16651.
WO2003073826-A2.
                                                                                                                                                                                                                                                         ACN44930 standard; DNA; 106378 BP.
Human genomic sequence hCG1742422.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP75188 standard; DNA; 276820 BP
Human ADAMTS2 gene.
WO2003031594-A2.
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12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
Hery Match 5.7%;
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(SAGR-) SAGRES DISCOVERY.
Best Local Similarity b
RESULT 1457
ID ADP6471 stand DE Human seque
PN WO2003 PD 04 PD 04 PA
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2003.
2003.
EV Match
Beet Local Similarity PRESULT 1464
ID AAL12012 stands
DB Human brear
PN W020015
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Best Local Similarity
RESULT 1466
ID ARK87086 standard; DN;
DE Human immune/haematopc
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
RESULT 1465
ID ACM82200 standard; DN
DE Breast cancer related
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PH
                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 1458
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Best Local Similarity
RESULT 1459
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1460
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Best Local Similarity
RESULT 1461
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ADJ10485 standard; DNA; 16509 BP.
Human isoprenylcysteine carboxyl methyltransferase genomic DNA SeqID 11.
US2003228688-A1.
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26474
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABA07813 standard; DNA; 32134 BP.
Human ovarian and breast cancer associated polynucleotide SEQ ID
WO200155325-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-DEC-2003.
(ISIS-) ISIS PHARM INC.
5.7%; Score 104.6; DB 12; Length 16509;
st Local Similarity 78.1%; Pred. No. 1.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD 30-MAX-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Query Match
Best Local Similarity 78.1%; Pred. No. 1.1e-21;
RESULT 1471
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5.7%; Score 104.6; DB 4; Length 32134;

it Local Similarity 78.1%; Pred. No. 2.7e-21;
                                                                                                                                                                                                                                     Length 2820;
                                                                                                                                                                                                                                                                          ID AAH18641 standard; cDNA; 3049 BP.

DB Human cDNA sequence SEQ ID NO:18867.

PN EP1074617-A2.

PD 07-FEB-2001.

PA (HELI-) HELIX RES INST.

Query Match 5.7%; Score 104.6; DB 4; Length 3049;

RESULT 1470
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                 unery Match 5.7%; Score 104.6; DB 6; Length 1568; Best Local Similarity 62.3%; Pred. No. 4.2e-22; RESULT 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AALO5543 standard; DNA; 8040 BP.
Human reproductive system related antigen DNA SEQ ID NO: 8231.
WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL03615 standard; DNA; 32134 BP.
Human reproductive system related antigen DNA SEQ ID NO: 6303.
WO200155320-A2.
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Human reproductive system related antigen DNA SEQ ID NO: 6304.
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                                                                                                                                                                                      18-SEP-2002.
(SHAN-) SHANGHAI INST ONCOLOGY.
STY MATCh 5.7%; Score 104.6; DB 10;
st Local Similarity 78.1%; Pred. No. 6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ETY MATCH 5.7%; Score 104.6; DB 4;
st Local Similarity 75.1%; Pred. No. 1.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G2-AUG-2001.
(HUWA-) HUMAN GENOME SCI INC.
5.7%; Score 104.6; DB 4;
ery Match imilarity 69.3%; Pred. No. 1.1e-21;
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ry Match
t Local Similarity 78.1%; Pred. No. 2.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE84040 standard; DNA; 7558 BP.
5' regulatory region of human gene BAK1.
WO2003044226-A2.
                                                                                                      ADF48653 standard; cDNA; 2820 BP.
Human PP7518 cDNA #SEQ ID 10.
CN1369505-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 1475
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24-APR-2002
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Best Local Si
RESULT 1469
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us-10-785-220b-11.rng.spdi

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12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
STY MATCH 5.7%; Score 104.6; DB 11; Length 129042;
st Local Similarity 72.7%; Pred. No. 6.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
ery Match 5.7%; Score 104.6; DB 12; Length 169659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7%; Score 104.6; DB 11; Length 110000; 79.8%; Pred. No. 5.6e-21;
                                      Score 104.6; DB 11; Length 75839;
Pred. No. 4.5e-21;
                                                                                                                                                                                                                                                                                     5.7%; Score 104.6; DB 12; Length 80928; 73.8%; Pred. No. 4.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ISIS-) ISIS PHARM INC.

5.7%; Score 104.6; DB 7; Length 98844;

t Local Similarity 78.1%; Pred. No. 5.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-2001.
(HELI-) HELIX RES INST.
ery Match 5.7%; Score 104.4; DB 4; Length 1427;
-- '-^al Similarity 68.8%; Pred. No. 4.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADUS9434 standard; DNA; 169659 BP.
Human cancer-associated (CA) gene sequence SEQ ID NO:70.
WO200458288-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ84099 standard; DNA; 98844 BP.
Human WRN (RECQL3) helicase genomic DNA - exons 1-20.
                                                                                                                                                                                                                                                                                                                                                                    Osteoarthritis-associated polymorphic nucleotide #88
                                                                                                 ADO25290 standard, DNA, 80928 BP.
Human protein kinase C iota/lambda genomic sequence.
WO2004041212-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                             (INCY-) INCYTE GENOMICS INC.
5.7%; Score 104.6; DB 10;
t Local Similarity 78.1%; Pred. No. 5.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABD32811 standard; DNA; 161051 BP.
Human cancer-associated genomic DNA HD16-063.
WO2004074320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA sequence SEQ ID NO:13802.
EP1074617-A2.
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Human genomic sequence hCG27276.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACN44014 standard; DNA; 370469 BP. Human genomic sequence hCG33130. W0200307386-A2.
                                                                                                                                                                                                                                                                                                                                                 ADL13556 standard; DNA; 95240 BP.
                                    Query Match 5.7%;
Best Local Similarity 78.1%;
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                   SAGRES DISCOVERY.
                                                                                                                                                               21-MAY-2004.
(SACK/) SACKTOR T C.
(CRAR/) CRARY J F.
(HERN/) HERNANDEZ A I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1494
                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1487
                                                                                                                                                                                                                                                                                                                                                                                         WO2003054166-A2.
03-JUL-2003.
                                                                                                                                                                                                                        (HERN/) HERNANDE
(MIRR/) MIRRA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200268690-A1.
                                                                                                                                                                                                                                                                  (SHAO/) SHAO C.
12-SEP-2003
(SAGR-) SAG
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                                                                                                                      Human ovarian and breast cancer associated polynucleotide SEQ ID NO 609.
                                                                                                                                                                                                                                                                                 AAKK4974 standard; DNA; 35871 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39786.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK74751 standard; DNA; 36485 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29563.
WO200157182-A2.
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AAK68958 standard; DNA; 36485 BP.
WO200157182-A2.
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Human geranylgeranyl diphosphate synthase 1 genomic DNA SeqID 11.
US2004005570-A1.
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sry Match
ir Local Similarity 78.1%; Pred. No. 3.5e-21;
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b. Samilarity 73.8%; Pred. No. 3.6e-21;
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                                                             DB 4; Length 32191;
                                                                                                                                                                                                                                                                                                                                                                                         4; Length 35871;
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Human cancer associated sequence HD10-013, SEQ ID 582.
WO2004060304-A2.
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Pred. No. 3.7e-21;
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ry Match

t. Local Similarity 76.6%; Pred. No. 2.9e-21;
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(HUMA-) HUMAN GENOME SCI INC.
(FUMA-) HUMAN GENOME SCI INC.
5.7%; Score 104.6; DB 4;
ery Match 76.6%; Pred. No. 2.9e-21;
                                                                                                                                                                                                                                                                                                                                        09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
6ry Match 5.7%; Score 104.6; DB 4
ery Match 78.1%; Pred. No. 2.8e-21;
                                                           5.7%; Score 104.6; DB 4 78.1%; Pred. No. 2.7e-21;
                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.

5.7%; Score 104.6; DB 4

5.0cal Similarity 78.1%; Pred. No. 2.7e-21;
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Human genomic sequence hCG20493.
WO2003073826-A2.
                                      (HUMA-) HUMAN GENOME SCI INC.
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(SAGR-) SAGRES DISCOVERY INC.
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Best Local Similarity
RESULT 1478
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Best Local Similarity
RESULT 1479
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Best Local Similarity
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RESULT 1481
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WO200155320-A2.
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Length 95240;

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ABK42351 standard; DNA; 10248 BP.
Genomic sequence #250 encoding novel human connective tissue polypeptide.
W0200155343-A1.
                                                                                                                                                                                                                                                                                                                                          DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36665.

PN W0200157182-A2.

PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 73.2%; Score 104.4; DB 4; Length 10248;

RESULT 1497

ID ADB60507 standard; DNA; 10248 BP.

DE Connective tissue related genomic DNA #250.

PN US2003054375-A1.

PN USAR-2003.

PA (HUMA-) HUMAN GENOME SCI INC.
AAK81852 standard; DNA; 3683 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36664.
WO200157182-A2.
                                                                                          DD 02-AUG-201.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 73.2%; Pred. No. 1.5e-21;

RESULT 1496

ID AAK81853 standard; DNA; 10248 BP.

DB Human immune/haematopoletic antine

PN W0200157182-A2.

PD 09-AUG-2001

PA (HIMA-) HUMAN GENOME SCI INC.

PN W0200157182-A2.

PD 09-AUG-2001
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Human autoimmune disease-related genomic DNA sequence - SEQ ID 1688
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20-MRZ-2003.
(HUMA-) HUMAN GENOME SCI INC.
Ery Match
From Similarity 73.2%; Pred. No. 1.5e-21;
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Human digestive system antigen genomic sequence SEQ ID NO: 4699.
WO200155314-A2.
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(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.7%; Score 104.4; DB 4; Length 14273;
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ry Match

t Local Similarity 73.2%; Pred. No. 8.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%;
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Best Local Similarity 7
RESULT 1498
ID ABA07392 standard; DNA
DE Human pancreatic cance
PN W020155206-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 7
RESULT 1499
ID AAK91123 standard; DNA
DE Human digestive system
PN W0200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME S
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Query Match
Best Local Similarity
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AF207907 Homo sapi
BD172325 Secreted
BD172325 Secreted
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BD173282 Secreted
BD173282 Secreted
BD175316 Secretory
BD075465 Secretory
AR410694 Sequence
AR43068 Sequence
AR526097 Sequence
AR526097 Sequence
AR526097 Sequence
AX69375 Sequence
AX69375 Sequence
AX69375 Sequence
AX69375 Sequence
AX69375 Sequence
AX69375 Sequence
AX69324 Sequence
AX69324 Sequence
AX69751 Sequence
AX69751 Sequence
AX6751 Homo sapi
AR0751 Homo sapi
AR0751 Sequence
CQ1831 Sequence
CQ1831 Sequence
CQ1831 Sequence
AR17239 Homo sapi
AR0751 Compositi
AR34150 Sequence
AR1739 Homo sapi
BD209704 Compositi
AR34101 Sequence
AR174005 Homo sapi
AR37101 Sequence
AR174005 Homo sapi
AR37101 Sequence
BD023444 Junction
AR301017 Sequence
BD0234198 Sequence
BD080011 Human F11
AR201017 Sequence
BD080011 Human F11
AR27698 Rattus no
AR27698 Rattus no
AR27698 Rattus no
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A91700 Sequence 4
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U89915 Mus musculu
BD061109 Secreted
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AR216156 Sequence
BCO46720 Xenopus 1
BCO82710 Xenopus 1
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A91702 Sequence 6
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AC087229 Mus muscu
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Rattus no
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Rattus no
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Ното варі
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Sequence
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AEF490407 F
AL162592 F
AL591806 F
AC111214 F
AR478943 S
CQ780520 S
BD125229 F
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BD080011
BC065309
AF276998
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A91700
BD023443
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A91702
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AC087229
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AR216156
BC046720
BC082710
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AX403735
AX454468
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AX490946
AX697527
AX358896
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AF154005
CQ781650
BD126359
AF111714
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AR478943
CQ780520
BD125229
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AL162592
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200822
217767
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-DB=denbmbl - OPMT=fastap - SUFFTX=p2n.rge - MINMATCH=0.1 -LOODEXX=0.
-UNITS=blts -START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=1500
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-USFR=US10785220 @cGN 1 1 3731 @runat 07092005 161055 11753 - NCPU=6 - ICPU=3
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BD175457 Secretory AR410836 Sequence AR439200 Sequence AR473220 Sequence AR577206 Sequence	AKS66239 Sequence AX098383 Sequence	BD075606 Secretory	BC065142 Mus muscu	AYS05340 Homo Bapı AYS05341 Mus muscu	BD172468 Secreted	BD173106 Secreted	BD173425 Secreted	BDI75459 Secretory	AR439202 Sequence	AR473222 Sequence	AR527208 Sequence	AR528627 Sequence	AR566241 Sequence	AX056647 Sequence	AX098387 Sequence	AX464218 Sequence	AX697702 Sequence	BD075608 Secretory	AY358288 Homo sapi	AX429017 Sequence	AY487418 Bos tauru	AR220843 Segmente	SACORD SERVICE	AXU/36/8 Sequence	AX429013 Sequence	AF195662 Mus muscu	BC029659 Mus muscu	AF315558 Mus muscu	CO598305 CACHAGO	COSSOS Seducince	AF334385 Kaccus no	AY005483 Mus muscu	AC151168 Bos tauru	AR220920 Sequence	BC033313 Mus muscu	M89650 Aplysia cal	M63437 Chicken KLG	CQ731799 Sequence	U88578 Drosophila	BS000002 Pan trog1	AR278799 Sequence	BD260118 Matrix-re	AB035511 Mus muscu	X67783 M.musculus	M84487 Mouse vascu	BC011159 Mus muscu	AY059393 Mus muscu	BC029823 Mus muscu	AF538326 Danio rer	CQ875263 Sequence	AF245505 Homo sapi	BC077626 Xenopus 1	AR282743 Sequence	CQ729908 Sequence	AF525411 Rattus no	AJ002535 Homo sapi	AL050303 Homo sapi	ADDORES MOMO GADI	AFOUSATO HOMO BADI	AL162851 Homo Bapi	AL163204 Homo sapi	AX747541 Sequence	AK092429 Homo sapi	BT011127 Drosophil	DIOCOCCE PROPORTION
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157.5 10.2 4191 9 157.5 10.2 4191 9 157.5 10.2 4193 6 157.5 10.2 4249 10 157.5 10.2 4249 10 157.5 10.2 4249 10 157.5 10.2 4249 10 157.5 10.2 4821 10 157.5 10.2 13793 9 157.5 10.2 13793 9 157.5 10.2 13793 9	157.5 10.2 177255 9 157.5 10.2 187235 2 157.5 10.2 196928 157 10.2 1952 6 157 10.2 1952 6 157 10.2 1952 9 157 10.2 4398 5	156.5 10.1 888 6 156.5 10.1 888 6 156.5 10.1 988 6 156.5 10.1 1446 10 156.5 10.1 2397 6 156.5 10.1 279	156.5 10.1 3637 10.1 156.5 10.1 3608 6 156.5 10.1 3808 9 156.5 10.1 3808 9 156.5 10.1 5336 5 156.5 10.1 6999 9 156.5 10.1 6999 9 156.5 10.1 6999 9 156.5 10.1 1339 6 156.5 10.1 10.1 10.1 10.1 10.1 10.1 10.1 10	156 10.1 1639 9 156 10.1 3087 10 156 10.1 3087 10 156 10.1 3613 10 156 10.1 5049 10 156 10.1 5749 9 156 10.1 4696 3 156 10.1 4696 3 156 10.1 294136 2 155 10.1 1638 10	1766 6 1766 6 1766 6 1708 10 1708 10 1708 10 1708 10 1709 1
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      GluValLysValLysLeuIleValLeuValProProSerLysProThrValAsnIlePro
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Gupta, S.Kant. and Pillarisetti, K.
Human Fl1 antigen: a novel cell sur
platelet aggregation
Patent: US 6558707-A 1 19-MAR-2002;
Location/Qualifiers
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                                                 further information.
human full ORF clones
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Fax: +49 30 32639 111

www.rzpd.de
   This clone is available from RZPD;
   conteat RZPD (customer.service@rzpd.de) for further information.
   This CDS clone is a part of a collection of human full ORF clones generated by RZPD.
   This CDS has been cloned incl. stopcodon.
   The CDS has been inserted into pDONR201 via a BP Clonase(TM)
   Traction. Additional sequence has been added in front of the stancedon: art. .AAAAAA GCA GGC (ATG).
   After the stop codon 3' UTR sequence is present in front of the att site (ACCCAGCTTTCTT).
   Compared to the reference sequence NM_144501 (gi21464106) we did not find any amino acid exchanges.
   Clone distribution: http://www.rzpd.de/products/orfclones/.
                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPD0834D0919D"
/clone_lbb="Human Full ORF Clones Gateway(TM) - RZPD"
/lab_host="DH10B"
/note="Vector: pDONR201, Site_1: attPl; Site_2: attP2"
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/protein_id="CAG38543.1"
/db_xref="G1:49065450"
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1 (bases 1 to 1140)
Gupta, S.K. and Pillarisetti, K.
Human Fil antigen as cell surface receptor participating in
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                        TyrSerArgGlyHisPheAspArgThrLysLysGlyThrSerSerLyslysVallleTyr
                                                                                        GAGTGGAAGTTTGACCAAGGAGACACCAGACTCGTTTGCTATAATAACAAGATCACA
                                                                                                                                          ArgGluAspThrGlyThrTyrThrCysMetValSerGluGlyGlyAsnSerTyrGly
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Patent: JP 2001509372-A 1 24-JUL-2001,
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24-JUL-2001
10-JUL-1998 JP 2000502080
10-JUL-1997 US 60/052186
SHALLEY KANT GUPTA, KODANDARAM PILLARISETTI
CIZNIS/09, A61K38/00, A61K39/395, A61K45/00, A61K48/00, A61P9/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 CCTGAGAATAATCCTGTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTTCTCCCCGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaSerTyrGluAspArgValThrPheLeuProThrGlyIleThrPheLysSerValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGlyGlyAsnSerTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           464 CGGGAAGACACTCGGGACATACACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluValLysValLysLeuIleValLeuValProProSerLysProThrValAsnIlePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerSerAlaThrIleGlyAsnArgAlaValLeuThrCysSerGluGlnAspGlySerPro
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                                                                                                                      PC C12N1/21,C12NS/10,C12P21/02,C12N1S/00,A61K37/02,C12NS/00
Human Fil antigen as cell surface receptor participating in C
platelet
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Mismatches:
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Matches:
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                                                                                                           GCTTCCTATGAGGACCGGGGGGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGAA
                                                                                                                                            ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGlyGlyBsnSerTyrGly
                                                                                                                                                                                                              GAGGICAAGGTCAAGGTCATGGTGCTTGTGCCTCCATCCAAGCCTACAGATTAACATCCCC
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Kornecki, E. and Sobocka, M.B.

Human platelet F11 receptor

Patent: US 6699688-A 1 02-MAR-2004;

Location/Qualifiers
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AR478942
AR478942.1 GI:47237803
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                                                                                                                                                           TyrSerargGlyHisPheaspargThrLysLysGlyThrSerSerLysLysVall1eTyr 280
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                                                                                                        AlaAlaValLeuValThrLeuIleLeuLeuGlyIleLeuValPheGlyIleTrpPheAla 260
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                   CCCATGACTTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAATGTGGGGGTCATCGTG
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                  MetGlyThrLysAlaGlnValGluArgLysLeuLeuCysLeuPhelleLeuAlalleLeu
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                                                      ProMetThrSerAsnAlaValArgMetGluAlaValGluArgAsnValGlyValIleVal
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Matches:
Conservative:
Mismatches:
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'note="unnamed protein product"
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T cell activating gene
Patent: WO 2004058805-A 67 15-JUL-2004;
Asahi Kasei Pharma Corporation (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                         CQ834196 1236 bp DNA Sequence 67 from Patent W02004058805. CQ834196 GI:50833733
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Best Local Similarity:
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PVKLIGGAYSGESPRVEWKEDGGGTTRLVCYNNKTTASYEDRYTFLETGTTFKSYTRE
DYGTYTCMVSEEGGNSYGEVKVKLIVLVPPSKPTVNIPSSATIGNAAULTGSEQDGSP
PSEYTWKROGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGY
GTPMTSNAVRMEAVERNUGYIVAAULVTLILLGILUFGINFAYSRGHFDRTKKGTSSK
KVIYSQPSARSEGEFKQTSSFLV"
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Ancea-Whatelet membrane glycoprotein, monoclonal antibody forces. Plained secretion and aggregation of human platelets by recognizing the F11 receptor, Method: conceptual translation with partial peptide sequencing"
                                                                                                                                                                                                                                                                                                                                      3 (bases 1 to 1822)
Sobocka, M.B., Sobocki, T., Rushbrook, J.I., Banerjee, P., Weiss, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein id="AAF22829.1"
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1 (Bases 100 to 175)
Naik, U.P., Ehrlich, Y.H. and Kornecki, E. Mechanisms of platelet activation by a stimulatory antibody: cross-linking of a novel platelet receptor for monoclonal antibody FII with the Fc gamma RII receptor
Biochem. J. 310 (Pt 1), 155-162 (1995)
                                                                                                                                                                                                                                                                                                                                                                                               and Cell Biology, SUNY, Health
Clarkson Ave., Brooklyn, NY 11203,
                                                                                                                                                                                              2 (bases 1 to 1822)
Sobocka, M.B., Sobocki, T., Banerjee, P., Weiss, C., Rushbrook, J.I.,
Norin, A.J., Hartwig, J., Salifu, M.O., Markell, M.S., Babinska, A.,
Ehrlich, Y.H. and Kornecki, E.
Cloning of the human platelet F11 receptor: a cell adhesion
molecule member of the immunoglobulin superfamily involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuCysSerLeuAlaLeuGlySerValThrValHisSerSerGluProGluValArgIle
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
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Direct Submission
Submitted (19-NOV-1999) Anatomy
Science Center at Brooklyn, 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                                                                                                 platelet aggregation
Blood 95 (8), 2600-2609 (2000)
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  GI:6653648
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Homo sapiens platelet F11 receptor mRNA, complete cds.
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(C12P21/02,C12R1:645),C12N15/00,C12N5/00
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Location/Qualifiers
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60/062846_24-0CT-1997_U

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1842)

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GENENTECH INC
OS Homo sapiens (human)
PN JP 2002223786-A/98
PD 13-AUG-2002
PF 18-DEC-2001 JP 2001385135
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JP 2002223786-A/98.
Homo sapiens (human)
Homo sapiens
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JEAN YUAN
C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC
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CC Secreted and transmembrane polypeptides and nucleic CC acid
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        ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGluGlyGlyAsnSerTyrGly 120

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/organism='Homo sapiens (human)'.
Location/Qualifiers
24-OCT-1997 US 60/063120,24-OCT-1997 US 60/06345,24-OCT-1997 US 60/06345,24-OCT-1997 US 60/063529,27-OCT-1997 US 60/063549,28-OCT-1997 US 60/063549,28-OCT-1997 US 60/06354,28-OCT-1997 US 60/06354,28-OCT-1997 US 60/06354,28-OCT-1997 US 60/06374,28-OCT-1997 US 60/06374,29-OCT-1997 US 60/06374,29-OCT-1997 US 60/06374,29-OCT-1997 US 60/06374,29-OCT-1997 US 60/063742,29-OCT-1997 US 60/06480,12-NOV-1997 US 60/06480,12-NOV-1997 US 60/066120,24-NOV-1997 US 60/066120,24-NOV-1997 US 60/066120,24-NOV-1997 US 60/066120,24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066453,25-NOV-1997 US 60/106473,25-NOV-1997 US 60/106470,25-NOV-1997 US 60/106473,25-NOV-1997 US 60/106473,25-NOV-1
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Conservative:
Mismatches:
Indels:
Gaps:
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    .1842
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Yuan,J.
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Homo sapiens (human)
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PC C12P21/02,C12P21/08//(C12P21/02,C12R1:91),(C12P21/02,C12R1:19), PC (C12P21/02,C12R1:645),C12N15/00,C12N5/00,C12N5/00,C12N5/00 CC Secreted and transmembrane polypeptides and nucleic CC acids encoding the
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Location/Qualifiers
                 60/063704, 29-0CT-1997 US 60/064215, 29-0CT-1997 US 60/064215, 29-0CT-1997 US 60/064219, 21-0CT-1997 US 60/064809, 12-NOV-1997 US 60/066286, 18-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/06645170, 24-NOV-1997 US 60/0664700, 24-NOV-1997 US 60/0664
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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Secreted and transmembrane polypeptides and nucleic acids encoding
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1. 1842
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1. (bases 1 to 1842)
Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.
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PN JP 2002238588-A/98
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C12N1/19,C12N1/21,C12N5/10//A61K38/00,A61K39/395,A61K39/395,
A61P43/00,
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I (bases 1 to 1842)
Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.
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C12N15/09,A61K45/00,A61P1/00,A61P13/12,A61P17/00,A61P17/06,
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                                      ProMetThrSerAsnAlaValArgMetGluAlaValGluArgAsnValGlyValIleVal
                                                     CCCATGACTTCAAATGCTGTGCGCATGGAAGCTGTGGGAAGCGGAATGTGGGGTCATCGTG
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TIN L GURNEY, AUDREY GODDARD,
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GENENTECH INC
OS Home capiens (human)
PN JP 2002253280-A/98
PD 10-SEP-2002
PF 18-DEC-2001 JP 2001385319
PR 17-SEP-1997 US 60/059122,17-SEP-1997 US
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transmembrane polypeptide
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BD175316.1 GI:29121012
JP 2002253280-A/98.
Homo sapiens (human)
Homo sapiens
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                       'organism='Homo

    .1842
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

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C12N12/9/09,C07K14/47,C07K14/705,C07K16/18,C07K16/28,C07K19/00,
C12N1/19,
C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02//(C12P21/08, PC
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AlaAlaValLeuValThrLeuIleLeuLeuGlyIleLeuValPheGlyIleTrpPheAla 260
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GENENTECH INC
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17-SEP-1997 US 60/0591
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JP 2001516580-A/98
02-OCT-2001
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BD075465.1 GI:22621068
JP 2001516580-A/98.
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Db 832 TATAGCCGAGGCCACTTTGACAAAAAAGGAAATTCGAGTAAGAAGGTGATTTAC 891  Qy 281 SerGlnProSerAlaArgSerGluGlyGluPheLyGlnThrSerSerPheLeuVal 299	NETWORDS SOURCE ONGANISM Unclassified.  NClassified.  NClassified.  NClassified.  NClassified.  NClassified.  NClassified.  NClassified.  NUclassified.  Numas.  Numas.	FEATURES Location/Qualifiers  SOURCE 1.1857  (organism="unknown" /mol_type="genomic DNA" /mol_type="ge	US-10-785-220B-1 (1-299) x AR410694 (1-1857)  QY  1 MetGlyThrLysAlaGlnValGluArgLysLeuLeuCysLeuPhelleLeuAlaileLeu 20	Oy 61 GlutrpLysPheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnLysIleThr 80	Qy         101 ArgGluAspThrTyThrCysMetValSerGluGluGlyGlyAsnSerTyrGly 120           Db         352 CGGGAAGACACTGGGACATACCTTGTATGGTCTCTGAGGAAGGCGCAACAGCTATGGG 411           Qy         121 GluValLysValLysLeuIleValLeuValProProSerLysProThrValAsnIlePro 140           Db         412 GAGGTCAAGGTCATGGTTGTGTTGTTGTTGTTGTGCTCCTCCAGGTTAACATCCCC 471           Qy         141 SerSerAlaThrIleGlyAsnArgAlaValLeuThrCysSerGluGlnAspGlySerPro 160           Db         472 TCCTCTGCCACCATTGGGAACCGGCAGTGCTGAACTCAGAACAAGATGCTTCCCA 531

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RESULT 3 US-09-907-794A-118 ; Sequence 118, Appl	; ORGANISM: Homo gapiens US-09-397-243D-1
Db 856 AGCCAC	; LENGTH: 1822 ; TYPE: DNA
Oy 281 SerGlr	SOFTWARE: Patentin Ver. 2.1
Db 796 TATAGO	; FALCA FILING ADATE: 1998-09-16 ; MIMBED OF EFO TO MOSC. 27
Oy 261 TyrSer	CONNENT AFFILICATION NOTION: 09/07/09/16430
Db 736 GCAGCC	FILE REFERENCE: 011.00221 CHRENT APPLICATION WIMBER: 115/09/397
Oy 241 AlaAla	; APPLICANT: Sobocka, marganata ; APPLICANT: Sobocka, Malgorata B
Db 676 CCCATC	; Falent NO. 0099000 ; GEDERAL NO. 0099000 ; ADDITANT FORMATION:
Oy 221 ProMet	US-09-39/-243D-1 ; Sequence 1, Application US/09397243D . Datath No. 620600
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Oy 201 ProLeu	Db 1004 AGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCCTGGTG 1060
) ) ) ) ) ) ) ) ) ) ) ) ) ) ) ) ) ) )	Oy 281 SerGlnProSerAlaArgSerGluGlyGluPheLysGlnThrSerSerPheLeuVal 299
Qy 181 ArgAla	Db 944 TATAGCCGAGGCCACTTTGACAGAACAAAGGAAGGGACTTCGAGTAAGAAGGTGATTTAC 1003
Db 496 CCTTC	Oy 261 TyrSerArgGlyHisPheAspArgThrLysLysGlyThrSerSerLysLysVallleTyr 280
Qy 161 Proses	Db 884 GCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAATCTTGGTTTTGGCATCTGGTTTGCC 943
  Db 436 TCCTCT	Qy 241 AlaAlaValLeuValThrLeuIleLeuLeuGlyIleLeuValPheGlyIleTrpPheAla 260
Qy 141 SerSer	
 	Ov 221 ProMetThrSerAsnAlaValArdMetGluAlaValGluArgAsnValGlvValIleVal 240
Qy 121 Gluyal	Db 764 CCCCTGTCAGCTCTGATACTGGAGAATACAGCTGTGAGGCACGGAATGGGTATGGGACA 823
    Db 316 CGGGAA	Qy 201 ProLeuSerAlaSerAspThrGlyGluTyrSerCysGluAlaArgAsnGlyTyrGlyThr 220
Qy 101 Argglu	Db 704 CGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACAACAGAGAGAG
Db 256 GCTTCC	Qy 181 ArgAlaPheSerAsnSerSerTyrValLeuAsnProThrThrGlyGluLeuValPheAsp 200
Qy 81 AlaSer	Db 644 CCTTCTGAATACACCTGGTTCAAAGATGGGATAGTGATGCCTACGAATCCCAAAAGCACC 703
Db 196 GAGTGC	Qy 161 ProSerGluTyrThrTrpPheLysAspGly1leValMetProThrAsnProLysSerThr 180
Qy 61 GluTri	Db 584 TCTCTGCCACCATTGGGAACCGGGCAGTGCTGACATGCTCAGAACAAGGTTCCCCA 643
Db 136 CCTGAC	Oy 141 SerSerAlaThr1leGlyAsnArgAlaValLeuThrCysSerGluGlnAspGlySerPro 160
Qy 41 ProGlu	Db 524 GAGGTCAAGGTCAACCTTCTGTGCCTCCATCCAAGCCTACAGTTAACATCCCC 583
OPLICATION OF THE TREE TREES OF THE TREES OF	Qy 121 GluValLysValLysLeulleValLeuValProProSerLysProThrValAsn1lePro 140
Qy 21 LeuCys	Db 464 CGGGAAGACACTGGGACATACACTTGTATGGTCTCTGAGGAGACGGCACACAGCTATGG 523
Db 16 ATGGGC	Qy 101 ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGlyGlyAsnSerTyrGly 120
Qy 1 MetGly	Db 404 GCTTCCTATGAGGACCGGGTGACCTTCTTGCCAACTGGTATCACCTTCAAGTCGGAAGAA 463
US-10-785-220B-1 (1-	Oy 81 AlaSerTyrGluAspArgValThrPheLeuProThrGlylleThrPheLysSerValThr 100
Query Match: DB:	Db 344 GAGTGGAAGTTTGACCAAGGAGACACCACCACTTGCTTTGCTATAATAACAAGATCACA 403
Percent Similarity: Best Local Similarit	Qy 61 GluTrpLysPheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnLysIleThr 80
S. Groot	Db 284 CCTGAGAATAATCCTGTGAAAGTTGTCCTGTGACTTACTT

Length:

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EXTYZGluASPAZGVAIThrPheLeuProThrGlyIleThrPheLySSerValThr 100
                                                                                                                                                                                                                                                                                          ralaThrIleGlyAsnArgAlaValLeuThrCysSerGluGlnAspGlySerPro 160
                                                                                                                                                                                                                                                                                                                                                                                                                    rGlunyrthrirpPhelysAspGlylleValMetProThrAsnProLysSerThr 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                            aPheSerAsnSerSerTyrValleuAsnProThrThrGlyGluLeuValPheAsp 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tThrserAsnAlaValArgMetGluAlaValGluArgAsnValGlyValIleVal 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aValLeuValThrLeuIleLeuLeuGlyIleLeuValPheGlyIleTrpPheAla 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LUASINASIPIOVALLYSLEUSErCYSAlaTyrSerGlyPheSerSerProArgVal 60
                                                                                                                                                                                                          plyspheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnLysIleThr 80
                                                                                | InproSerAlaArgSerGluGlyGluPheLysGlnThrSerSerPheLeuVal 299
299
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                            1-299) x US-09-397-243D-1 (1-1822)
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SerSerAlaThrIleGlyAsnArgAlaValLeuThrCysSerGluGlnAspGlySerPro 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GluValLysValLysLeuIleValLeuValProProSerLysProThrValAsnIlePro 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472 TCCTCTGCCACCATTGGGAACCGGGCAGTGCTGACATGCTCAGAACAAGATGGTTCCCCA 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          772 GCAGCGGTCCTTGTAACCCTGATTCTCCTGGGAATCTTGGTTTTTGGCATCTGGTTTGCC 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrserArgGlyHisPheAspArgThrLysLysGlyThrSerSerLysLysVallleTyr 280
                                                                                                                                                                                                                                                                                                    81 AlaSerTyrGluAspArgValThrPheLeuProThrGlyIleThrPheLy8SerValThr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 GCTTCCTATGAGGACCGGGGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGlyGlyAsnSerTyrGly 120
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                                                                                                                                                                                                                                                     52 ATGGGGACAAAGGCGCAAGTCGAGAAGAGTGTTGTGCCTCTTCATATTGGCGATCCTG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgAlaPheSerAsnSerSerTyrValLeuAsnProThrThrGlyGluLeuValPheAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                    172 CCTGAGAATAATCCTGTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GluTrpLysPheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnLysIleThr
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                                                                                                                                                    US-10-785-220B-1 (1-299) x US-09-907-794A-118 (1-1857)
Matches:
Conservative:
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Indels:
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; Sequence 118, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
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                            Percent Similarity:
Best Local Similarity:
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                                                                           Query Match:
DB:
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CURRENT FELING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US/09/907,794A
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-36
PRIOR APPLICATION NUMBER: PCT/US99/2814
PRIOR APPLICATION NUMBER: PCT/US99/2814
PRIOR APPLICATION NUMBER: PCT/US99/2814
PRIOR APPLICATION NUMBER: PCT/US99/2814
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-03
PRIOR PELING DATE: 1999-1
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Grimaldi, Christopher
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Wood, William, I.
                                                                                                                               Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                                                                                                                        Gerritsen, Mary E.
Goddard, A.
                                                                                                                                                                                                      Gao, Wei-Qiang
Gerber, Hanspeter
Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                 Sherman
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US-09-907-794A-118
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411

231

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80

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220

Alignment Scores: Pred. No.:

651

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261 TyrSerArgGlyHisPheAspArgThrLysLysGlyThrSerSerLysLysVallleTyr 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      712 CCCATGACTTCAAATGCTGTGCGCATGGAAGCTGTGGGGGGAATGTGGGGGGTCATCGTG 771
                                                                                                                                                                                             52 ATGGGGACAAAGGCGCAAGTCGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerGInProSerAlaArgSerGluGlyGluPheLyBGlnThrSerSerPheLeuVal 299
                                                                                                                                                                                                                                                    172 CCTGAGAATAATCCTGTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  532 CCTTCTGAATACACCTGGTTCAAAGATGGGATAGTGATGCCTACGAATCCCAAAAGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     832 TATAGCCGAGGCCACTTTGACAGAACAAAGGAAGGGACTTCGAGTAAGAAGGTGATTTAC
                                                                                                                                                                   1 MetGlyThrLygAlaGlnValGluArgLysLeuLeuCysLeuPheileLeuAlaIleLeu
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                         Conservative:
Mismatches:
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        Matches:
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    1544.00
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Best Local Similarity:
Query Match:
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US-09-902-775A-118
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PRIOR FILING DATE: 1999-0-26 OF 100 OF
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                                                                                                                                                                                                                                                Godowski, Paul J.
Grimaldi, Christopher
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pan, James
Roy, Margaret Ann
Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc.
Eston, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
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US-09-905-125A-118
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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100 351 120 411 140

291

80

171

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231

9

160 531 180

471

240

891

1857

Length:

2.12e-176

Alignment Scores: Pred. No.:

200

651

591

9

80

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81 AlaSerTyrGluAspArgValThrPheLeuProThrGlylleThrPheLysSerValThr 100
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     Matches:
Conservative:
Mismatches:
Indels:
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     1544.00
100.00%
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                      Percent Similarity:
Best Local Similarity:
Query Match:
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/902,775A

CURRENT FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: PCT/USO0/04414

PRIOR APPLICATION NUMBER: PCT/USO0/04414

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR PLILING DATE: 1999-07-26

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PRIOR APPLICATION NUMBER: US 60/146,222

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PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/21697

PRIOR APPLICATION NUMBER: PCT/US99/21697

PRIOR APPLICATION NUMBER: PCT/US99/21697

PRIOR FILING DATE: 1999-00-15

PRIOR PLILING DATE: 1999-01-15

PRIOR FILING DATE: 1999-11-20

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR PLILING DATE: 1999-11-20

PRIOR APPLICATION NUMBER: PCT/US99/28664

PRIOR APPLICATION NUMBER: PCT/US99/28016

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR PLILING DATE: 1999-11-20

PRIOR PLILING DATE: 1999-11-20

PRIOR PLILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR PLILING DATE: 1999-12-02

PRIOR PLILING DATE: 1999-12-06

PRIOR PLILING DATE: 1999-12-07

PRIOR PLILING DATE: 1999-12-07
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Gerber, Hanspeter
Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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ORGANISM: Homo sapiens
US-09-902-775A-118
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160

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US-09-906-700-118
; Sequence 118, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:

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1857

Length:

2.12e-176

Matches:

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APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, Jinkoha P.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Michola F.
APPLICANT: Wasgaret Ann
APPLICANT: Wood, Milliam, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Society Profession of Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Society Profession of Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Society Profession of Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Society Profession of Transmembrane Polypeptides and Nucleic
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TITLE OF INVENTION: Society Profession of Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Society Profession of Transmembrane Polypeptides and Nucleic
TRANSMERS PRICATION NUMBER: US 60/145, 208
RRIOR PLILICATION NUMBER: DC7/1899/2019
RRIOR PLILICATION NUMBER: PC7/1899/2119
RRIOR PLILICATION NUMBER: PC7/1899/2119
RRIOR PLILICATION NUMBER: PC7/1899/2119
RRIOR PLILICATION NUMBER: PC7/1899/21011
RRIOR PLILICATION NUMB
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Grimaldi, Christopher
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wel-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth, J.
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Filvaroff, Ellen
Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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US-09-906-700-118
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Length:

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                                                                                                                              GluValLysValLysLeuIleValLeuValProProSerLysProThrValAsnIlePro 140
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               Conservative:
Mismatches:
Indels:
                                                                                               US-10-785-220B-1 (1-299) x US-09-906-700-118 (1-1857)
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US-09-903-603A-118
Sequence 118, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
 1544.00
100.00%
100.00%
           Percent Similarity:
Best Local Similarity:
Query Match:
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Percent Similarity:
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Query Match:
DB:
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APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acide Encoding the Same
CURRENT APPLICATION NUMBER: UG/09/903,603A
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: DG/0145,698
PRIOR APPLICATION NUMBER: DG/0146,229
PRIOR APPLICATION NUMBER: OG/0146,294
PRIOR APPLICATION NUMBER: OG/0146,222
PRIOR APPLICATION NUMBER: OG/0146,222
PRIOR APPLICATION NUMBER: OG/0146,222
PRIOR APPLICATION NUMBER: PG/US99/20594
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PG/US99/20594
PRIOR APPLICATION NUMBER: PG/US99/20594
PRIOR APPLICATION NUMBER: PG/US99/20594
PRIOR APPLICATION NUMBER: PG/US99/20594
PRIOR APPLICATION NUMBER: PG/US99/20319
PRIOR PLING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PG/US99/20319
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-11-20
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Grimaldi, Christopher
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                            Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
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Stewart, Timothy A.
                                                                                                                                                      Gerber, Hanspeter
Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                      Pan, James
Paoni, Nicholas F.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                         Wei-Qiang
                                                                                                                                                                                                   Goddard, A.
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; ORGANISM: Homo sapiens
US-09-903-603A-118
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                                                                                                                                                                       1 MetGlyThrLysAlaGlnValGluArgLysLeuLeuCysLeuPhelleLeuAlalleLeu
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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US-09-904-920A-118
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APPLICANT: Kljavin, Vari J.
APPLICANT: Kljavin, Vari J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, Jamen P.
APPLICANT: Pan, Jamen P.
APPLICANT: Pan, Jamen P.
APPLICANT: Pool, Micholas F.
APPLICANT: Pool, Milana, P. Mickey
APPLICANT: Wan Millana, P. Mickey
APPLICANT: Wan Millana, P. Mickey
APPLICANT: Wand, Williana, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION NUMBER: US 60.143, 048
PRIOR FILING DATE: 1999-07-36
PRIOR PLICATION NUMBER: US 60.146, 222
PRIOR PLICATION NUMBER: PCT/US99/20194
PRIOR PLICATION NUMBER: PCT/US99/2014
PRIOR PLICATION NUMBER: PCT/US99/2014
PRIOR PLICATION NUMBER: PCT/US99/2014
PRIOR PLICATION NUMBER: PCT/US99/3019
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Grimaldi, Christopher
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Hillan, Kenneth, J.
Kijavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
   Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
                                                                                                                                    Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Goddard, A.
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; ORGANISM: Homo sapiens
US-09-904-920A-118
                                                            APPLICANT:
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Length:

2.12e-176

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ProserGlutyrThrTpPheLysAspGlyIleValMetProThrAsnProLysSerThr 180
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                                                                                                                                                      1 MetGlyThrLysAlaGlnValGluArgLysLeuLeuCysLeuPheIleLeuAlaIleLeu
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                  Conservative:
Mismatches:
Indels:
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; Sequence 118 Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
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RESULT 10
US-09-905-381A-118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THILK DOF INVENTION: ACLIGE ENCORING CIRC SCHOOL TIER REPERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/909,064

CURRENT FILING DATE: 2001-07-18

PRIOR PELING DATE: 2000-02-22

PRIOR PELING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIO
                                                                                                                                                                                                                                       Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                                                                                                                                                        Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timcthy A.
Tumas, Daniel
                                                                                     Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
                                                                                                                                                                Gao, Wei-Qiang
Gerber, Hanspeter
                                                                                                                                                                                                                   Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                             Kljavin, Ivar J.
Mather, Jennie P.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
                                                                   Eaton, Dan L.
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ORGANISM: Homo
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APPLICANT:
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Length:

2.12e-176

Alignment Scores: Pred. No.:

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81 AlaSerTyrGluAspArgValThrPheLeuProThrGlyIleThrPheLysSerValThr 100
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Mismatches:
Indels:
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     Matches:
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                             Percent Similarity:
Best Local Similarity:
Query Match:
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221 ProMetThrSerAsnAlaValArgMetGluAlaValGluArgAsnValGlyValIleVal 240
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Matches:
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1544.00
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Best Local Similarity:
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US-09-906-618-118
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APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, Micholas F.
APPLICANT: Tumas, Janiel
APPLICANT: Wood, Milliam, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Nucleic 2000-07-18
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Society 2000-07-18
THOR APPLICATION NUMBER: US 60/145, 698
PRIOR APPLICATION NUMBER: US 60/146, 222
PRIOR PAPLICATION NUMBER: PCT/US99/2009
PRIOR FILING DATE: 1999-0-16
PRIOR PLING DATE: 1999-0-16
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-2
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                                                                                                                                                                                                                                                        Godowski, Paul J.
Grimaldi, Christopher
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Hillan, Kenneth, J.
Kijavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                        Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                Gerritsen, Mary E
                                                                                                                                                                                            Gerber, Hanspeter
  Genentech, Inc.
Ashkenazi, Avi
Botstein, David
                                                                Desnoyers, Luc
Eaton, Dan L.
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; ORGANISM: Homo
US-09-905-381A-118
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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411

231

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291

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160

471

180

200

651

711

1857

Length:

2.12e-176

Alignment Scores: Pred. No.:

591

Conservative: Mismatches: Indels:

Matches:

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1544.00
100.00%
100.00%
100.00%
          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ## APPLICANT: Tunnas, Daniel
## APPLICANT: Williams, Daniel
## APPLICANT: Williams, Daniel
## APPLICANT: Wood, Williams, Daniel
## TITLE OF INVENTION: Acide Encoding the Same
FILIS OF THING DATE: 2001-07-16
## PRIOR APPLICATION NUMBER: US/09/906,618
## PRIOR APPLICATION NUMBER: US/01/41,048
## PRIOR APPLICATION NUMBER: US/01/41,048
## PRIOR PILING DATE: 1999-07-20
## PRIOR APPLICATION NUMBER: US/01/46,22
## PRIOR APPLICATION NUMBER: US/01/46,22
## PRIOR PILING DATE: 1999-07-26
## PRIOR PILING DATE: 1999-07-26
## PRIOR PILING DATE: 1999-07-26
## PRIOR PILING DATE: 1999-09-13
## PRIOR PILING DATE: 1999-09-13
## PRIOR PILING DATE: 1999-09-13
## PRIOR PILING DATE: 1999-09-15
## PRIOR PILING DATE: 1999-10-36
## PRIOR PILI
                                                                                                                                                                                                       Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Paoni, Nicholas F.
                                                                                                                                                                  Gao, Wei-Qiang
Gerber, Hanspeter
Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                               Fong, Sherman
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; ORGANISM: HOMO
US-09-906-618-118
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1857

Length

2.12e-176

Alignment Scores:

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240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGGAAGACACTGGGACATACACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGG
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                                                                                                                                                                                                                    MetGlyThrLysAlaGlnValGluArgLysLeuLeuCysLeuPheIleLeuAlaIleLeu
                                                                                                                                                                                                                                                                                 52 ATGGGGACAAAGGCGCAAGTCGAGAGAACTGTTGTGCCTCTTCATATTGGCGATCCTG
                                                                                                                                                                                                                                                                                                                         LeuCysSerLeuAlaLeuGlySerValThrValHisSerSerGluProGluValArgIle
                                                                                                                                                                                                                                                                                                                                                                                         112 TIGIGCICCCIGGCALIGGGCAGIGLIACAGIGCACTCITCIGAACCIGAAGICAGAATI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GluValLysValLysLeuIleValLeuValProProSerLysProThrValAsnIlePro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 ArgAlaPheSerAsnSerSerTyrValLeuAsnProThrThrGlyGluLeuValPheAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCCTGTCAGCCTCTGATACTGGAGAATACAGCTGTGAGGCACGGAATGGGTATGGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                              ProGluAsnAsnProValLysLeuSerCysAlaTyrSerGlyPheSerSerProArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTTCTGAATACACCTGGTTCAAAGATGGGATAGTGATGCCTACGAATCCCAAAAGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProLeuSerAlaSerAspThrGlyGluTyrSerCysGluAlaArgAsnGlyTyrGlyThr
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299
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                                                                                                                                                                  US-10-785-220B-1 (1-299) x US-09-906-618-118 (1-1857)
                                                                                                                 Gaps:
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; Patent No. 6150502
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-188-930-254
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CCCATGACTTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAATGTGGGGGTCATCGTG
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1536.00
99.67%
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Mouse
US-09-312-283C-254
                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                           261
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steaman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Ontue! Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Land Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2.74
LENGTH: 1421
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Best Local Similarity:
Query Match:
DB:
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; ORGANISM: Human
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| Sequence 254, Application US/09312283C
| Patent No. 6573055
| GENERAL INFORMATION:
| APPLICANT: Strachan, Lorna
| APPLICANT: Strachan, Lorna
| APPLICANT: Murison, James D.
| APPLICANT: Murison, James G.
| TITLE OF INVENTION: Compositions Isolated from Ski:
| TITLE OF INVENTION: Murison Government of Treir Use
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Sequence 70, Application US/09188930A
Sequence 70, 6120502
GENERAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Steeman, Matthew
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000-11011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 70 LENGTH: 1421
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US-09-312-283C-70
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Human DNA40628 cDNA encoding PRO301 protein.
US2003171568-A1.
                                                                                                                                                                                                                                                                                                                                                        ADK40842 standard; cDNA; 1822 BP.
DNA encoding human platelet F11 receptor #1
US6699688-B1.
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Human cDNA clone DNA40628 encoding PRO301.
WO9914241-A2.
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Full length human F11 receptor cDNA Seq 6.
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WO9914328-A2.
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y Match: 100.00% Inde
                                                                                                                            Human polynucleotide SEQ ID NO 1261. 89-00190304-A2.
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PA (HUMA-) HUWAN GENOME SCI INC.
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PA (GETH) GENENTECH INC.
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DE DNA encoding hum
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-Q=(cgn2_1/USPTO_spool/USL0785220/runat_07092005_161118_12038/app_query.fasta_1.455
-Q=(cgn2_1/USPTO_spool/USL0785220/runat_07092005_161118_12038/app_query.fasta_1.455
-DB=N_Geneseq_16Deco4_oFPMT=fastagp_SUFFIX=p2n.rng_-MNNMATCH=0.1_-LCOPCL=0
-LCOPEXT=0_-UNITS=bits_-START=1_-END=-1_-MATRIX*=blosum62_-TRANS=human40.cdi
-LIST=1500_-DOCALIGN=200_-THR_SCORE=pct_-THR_MAX=100_-THR_MINEN=0_-ALIGN=1500
-WODE=LOCAL_OUTFWT=pto_-NORM=ext_-HRAPSIZE=$500_-MNLLEN=0_-AMZIEN=200000000
-USRR=USR10785220_@CGN_1_1_470_@runat_07092405_161118_12038_-NCFU=6_-ICFU=3
-NO_WARP_-LARGEQÜERY_-NEG_SCORES=0_-WAIT_-DSPBLOCK=100_-LONGLOG
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GenCore version 5.1.6

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OM protein - nucleic search, using frame plus p2n model

Run on: September 8, 2005, 20:54:18 ; Search time 638 Seconds

(without alignments)

2774.299 Million cell updates/sec
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters:
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DE F11 antigen coding se
PN W09902561-A1.
PD 21-JAN-1999.
PA (SMIK ) SMITHKLINE BE
Percent Similarity: 10
Query March: 10
RESULT 3
ID ADQ9589 standard; CD
ID ADQ9589 trandard; CD
ID ADQ9589 trandard; CD
IN W02004058805-A2.
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PD 30-JAN-2003.
PA (ELIL ) LILLY & CO EL Percent Similarity: 10 Best Local Similarity: 10 RESULT 2
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Percent Similarity: Best Local Similarity: Query Match:	standard; 0301 gene 11105-A2. 004. GENENTECH larity: Imilarity:	standard creted/tr 7561-A1. GON. GENENTECH arity:	RESULT 13  TO AAZ52204 standard; DE Human PRO301 prote PN WO200015797-A2. PD 23-MAR-2000. PA (GETH ) GENENTECH Percent Similarity; Best Local Similarity; Query Match:	RESULT 14 ID AAAA7581 standard; DE Human PRO301 CDNA s PN WO20003221-A2. PD 08-JUN-2000. PA (GETH) GENENTECH I Percent Similarity: Best Local Similarity: Query Match:	KESULT 15 ID AAA49723 standard; DE Human PRO301 CDNA PN WO200037638-A2. PD 29-UNN-2000. PPA (GETH ) GENENTECH Percent Similarity; Best Local Similarity; Query Match:	KESULI 16 ID ADC78438 standard; DE Human PRO301 cDNA. PN W0200015796-A2. PD 23-WAR-2000. PA (GETH) GENEWECH Percent Similarity: Best Local Similarity: Query Match:	772393 standard, aan PRO301 cDNA. ONO.104311-A1. JAN.2001. TTH ) GENENTECH Similarity: al Similarity:	KESULT ID AAC87026 standard; of DE Nucleotide sequence PN W0200077037-A2. PD 21-DEC-2000. PA (GETH) GENENTECH II PETCENT SIMILATIV:

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AAC97460 standard; cDNA; 1857 BP.
Human angiogenesis-associated protein PRO301 cDNA, SEQ ID NO:118.
WO200053753-A2.
                                                  (UNQ264).
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Human cDNA for secreted/transmembrane protein PRO301
US2003003530-A1.
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Human cDNA sequence encoding for PRO301 polypeptide.
WO200140466-A2.
07-JUN-2001.
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        Indels:

        RESULT 19
        IDD AASO0159 standard; cDNA; 1857 BP.

        DE Human cDNA clone DNA40628-1216 encoding PRO301

        PN WO200119991-A1.

Mismatches:
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RESULT 25
ID ACD07497 standard; CDNA; 1857 BP.
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PN W0200119991-n..

PD 22-MAR.2001.

PA (GETH ) GENENTECH INC.

Percent Similarity: 100.00%

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Ouery Match: 100.00%
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PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
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PAONI N F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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PA (MARS) MARSTERS S A

PA (PANJ) PAN J.

PA (PANJ) PAN J.

PA (STEP) STEPHAN J F.

PA (WATA) WATANABE C K

WHILL) WILLIAMS P M

PA (WOLL) WOOD W I.

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RESULT 22
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INC. 100.00% 100.00% 100.00%	dard; cDNA; 1857 BP. human PRO polypeptide	H INC. 100.00% : 100.00%	NA; 1857 secreted/	INC. 100.00\$ 100.00\$ 100.00\$	CDNA; 1857 BP. ed and transmembrane	INC. 100.00\$ 100.00\$ 100.00\$		INC. 100.00\$ 100.00\$	CDNA; 1857 BP secreted and	INC. 100.00\$ 100.00\$ 100.00\$		INC. 100.00% 100.00% 100.00%	cDNA; 1857 BP nsmembrane pro	INC. 100.00\$ 100.00\$ 100.00\$
PD 26-DEC-2002. PA (GETH ) GENENTECH Percent Similarity: Query Match:	stan oding	· 5 >-	standar NA encod 2240-A1.	002. GENENTECH arity: milarity:	RESULT 28 ID ACA04985 standard; CDNA; DE Novel human secreted and PN US2003032063-A1.	ous. GENENTECH arity: milarity:	DE Human secreted/transmembrane PN US2003044839-A1.	PD 06-MAR-2003. PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	DE DNA encoding novel PN US2003017563-A1.	003. GENENTECH arity: milarity:	KESULI 31  ID ACD41977 standard; cDNA; 185' DE Human secreted/transmembrane PN US2003036179-A1.	0003. GENENTECH arity: milarity:	KESULI 32 ID ARX66114 standard; cDNA; 1857 BP. DE Human secreted/transmembrane protein PN US2002160314-Al.	PD 51-UCT-2002. PD 51-UCT-2002. Percent Similarity: Best Local Similarity: Query Match:

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Human cDNA encoding a secreted/transmembrane protein, SEQ ID 365.
US20030312155-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003017463-A1.
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MA45884 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003022328-A1.
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Novel human secreted and transmembrane protein PRO301 DNA.
US2003032062-A1.
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US2003032057-A1.
13-PEB-2003.
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Human secreted / transmembrane polypeptide PRO301 cDNA.
US2003036060-A1.
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US2003023054-A1.
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ACA65646 standard; cDNA; 1857 BP.
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US2002177165-A1.
28-NOV-2002.
(GETH ) GENENTECH INC.
cent Similarity: 100.00$
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DE Human PRO Dolyuncleocide #183.

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100.00	ID ADA94029 standard; cDNA; 1857 BP.  DE Human PRO polynucleotide #183.  PN US200307722-A1.  PD 24-APR-2003.  PA (GETH) GENENTECH INC.  Percent Similarity: 100.00% Mismatches: 0  Query Match: 100.00% indels: 0	ID ADB19925 standard; cDNA; 1857 BP.  DE Novel human secreted and transmembrane protein PRO301 CDNA.  PN US2003082691-A1.  PD 01-MAY-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 100.00% Mismatches: 0  Query Match: 100.00% Indels: 0	ID ADB13237 standard; cDNA; 1857 BP.  ID ADB13237 standard; cDNA; 1857 BP.  DE Human PRO polymucleotide #183.  PN US2003082710-A1.  PD 01-MAY-2003.  PA (GETH) GENENTECH INC.  Percent Similarity: 100.00% Mismatches: 0  Query Match: 100.00% Indels: 0	RESULT 69  ID ACD98606 standard; CDNA; 1857 BP.  ID NOVE1 human secreted and transmembrane protein PRO301 cDNA.  DE NOVE1 human secreted and transmembrane protein PRO301 cDNA.  PN US2003044945-A1.  PD 06-MAR-2003.  PA (GETH ) GENEWTECH INC.  Percent Similarity: 100.00% Mismatches: 0  Duerv Match: 0  Ouerv Match: 0  Ouerv Match: 0  Ouerv Match: 0	1 standard; CDNA; 1857 BP.  RO polynuclectide #183. 2003. GENENTECH INC. Larity: 100.00\$ Conservative: imilarity: 100.00\$ Mismatches: 100.00\$ Indels:	2299 standard; cDNA; 1857 BP. 03054401-A1. AR-2003. H) GENEWTECH INC. imilarity; 100.00\$ ch: Similarity: 100.00\$	RESULY 72 ID ADB24724 standard; CDNA; 1857 BP. DE Human PRO polynucleotide SEQ ID NO 365. PN US2003077713-A1. PD 24-APR-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Querry Match: 100.00\$ Indels: 0	DE: Human, PRO polynucleotide #183.  DE: Human, PRO polynucleotide #183.  PN 01-003082701-A1.  PD 01-MAY-2003.  PA (GETH ) GENENTECH INC:  Percent Similarity: 100.00\$ Conservative: 0  Best Local Similarity: 100.00\$ Mismatches: 0
000	RO301 CDNA.		· • • • •	o o o	CO301 CDNA.		CDNA.	
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Percent Similarity: Best Local Similarity: Odery Match:	ACACH Search Standard; CDNA; 1857 BP.  DE Novel human secreted and transmembrane protein PN US2003087345-A1.  PD 08-MAY-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 100.00\$ Mismatches: Ouery Match: 100.00\$ Indels:	RESULT 59  1D ADB16698 standard; CDNA; DE Human PRO polynuclectide PN US2003087349-A1. PD 08-MAY-2003. PA (GETH ) GRNENTECH INC. Percent Similarity: 100.00 Destry Marchy Similarity: 100.00	REGIT 60  ID ACD83048 standard, CDNA; DE Human PRO polynucleotide PN US2003044793-A1. PD 06-WAR-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 100.00 Dest Local Similarity: 100.00	Query Macch:  Query Macch:  ID July 61  ID ADA16154 standard; CDNA; 1857 BP.  E Human secreted/transmembrane protein CDNA, PN US2003049521-A1.  PN US2003049521-A1.  PA (GETH) GENENTECH INC.  PA (GETH) GENENTECH INC.  Percent Similarity: 100.00% Mismatch  Best Local Similarity: 100.00% Mismatch	Query Match: 100.00\$ Indels: RESULT 62 ID ADA91790 standard; cDNA; 1857 BP. DE Novel human secreted and transmembrane protein PN US2003082694-A1. PD 01-MAY-2003. PA (GETH ) GENENTECH INC. PA (GETH ) GENENTECH INC. Percent Similarity: 100.00\$ Conservative. Best Local Similarity: 100.00\$ Mismatches:	Query Match: RESULT 63  BESULT 63  D ADB14853 standard; CDNA; DE Human PRO polynucleotide PN US2003087351-A1. PD 08-MAY-2003. PA (GETH) GENENTECH INC. Percent Similarity: 100.00	Query Match:  Query Match:  LD ADA47262 standard; CDNA; 1857 BP.  LD Human secreted/transmembrane polypeptide PR0301  PN US200304844-A1.  PD 06-MAR.2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 100.00\$ Mismatches:  Query Match: 100.00\$ Indels:	RESULT 65 ID ADB18814 standard; CDNA; 10 DE Novel human secreted and the US2003073211-A1. PD 17-APR-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 100.00%

ğ	5 # # 5		PD 24-APR-2003. PA (GETH ) GENENTE Percent Similarity: Best Local Similarity:	ŽŽ.	ID ADECELU SCANDA DE CDNA encoding h PN US2003092147-A1 PD 15-MAY-2003	ပ္ပို္န	Query Match: RESULT 85.007 21222		PA (GETH ) GENENTE Percent Similarity:	Best Local Similarit Query Match:	RESULT 86 ID ADA61025 standa	DE Homo sapiens. PN US2003049817-A1 PD 13-MAR-2003.	PA (GETH) GENENTE Percent Similarity: Best Local Similarit	Query Match: RESULT 87	ADB241/2 Human PF US200307 24-APR-2	PA (GEIH ) GENENIE Percent Similarity: Best Local Similarit	Query March: RESULT 88 ID ADA96501 standa	DE Human PRO polyn PN US2003082690-A1 PD 01-MAY-2003	St.		PA (GETH ) GENENTE Percent Similarity: Best Local Similarit	Query Match: RESULT 90
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Query Match: 100.00 RESULT 74 ID ADA75211 standard; cDNA; DE Human PRO polynucleotide	PN US2003073216-A1. PD 17-APR-2003. PA (GETH) GENENTECH IN Percent Similarity: 1 Best Local Similarity: 1 Query Match: 1	RESULT 75 ID ADABS289 standard, cDNA, 1857 BP. DE Novel human secreted and transmembrane protein PRO301	PN US2003082695-A1. PD 01-MAY-2003. PA (GETH) GENENTECH INC. Percent Similarity: 100	Best Local Similarity: Query Match:	KESULI 16 ID ADA84737 standard; CDNA; 1857 BP DE Novel human secreted and transmer PN 1152001308-11	PD 01-MAY-2003. PA (GETH ) GENENTECH	Best Local Similarity: Query Match:	ID ACD23226 standard; cDNA; 1857 BP BP Human PRO polynucleotide #21.	PD 03-APR-2003. PD (GETH ) GENENTECH INC.	Percent Similarity: Best Local Similarity:	Query Match: RESULT 18	ID ADB29993 standard; cDNA; 1857 BP. DE cDNA encoding human PRO polypeptide #183 PN US2003073214-A1.	PD 17-APR-2003. PA (GETH ) GENENTECH INC Percent Similarity: 100	Best Local Similarity: Query Match:	RESULT 79 ID ADA80521 standard; cDNA; 1857 BP. DE Human PRO polynucleotide #183. PN US2003082761-A1.	, ö	Best Local Similarity: Query Match: RESULT 80	ID ADA75763 standard; cDNA; 1857 BP. DE Human PRO polynucleotide #183. PN US2003082703-A1.	PD 01-TMAT-2003. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	RESULT 81 ID ADA46988 standard; CDNA; 1857 BI DE Human PRO polynucleotide #183. PN US2003073210-A1.	, ü	Best Local Similarity: Query Match:

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Human secreted/transmembrane protein cDNA, #25.

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ADB21743 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
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Novel human secreted and transmembrane protein PRO301 CDNA.
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CDNA encoding human PRO polypeptide #183
US2003082760-A1.
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US2003077710-A1.
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          ADA95949 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003082759-A1.
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DE Human PRO polynucleotide #183.
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AUABBU48 standard; CDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 CDNA.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003054516-A1.
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ID ADA88600 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
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ID ADB28466 standard; CDNA; 1857 BP.
DE CDNA encoding human PRO polypeptide #183.
PN US2003082699-A1.
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ID ADB29018 standard; CDNA; 1857 BP.
DE CDNA encoding human PRO polypeptide #183.
PN US2003082706-A1.
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RESULT 101
ID ADA17222 standard; cDNA; 1857 BP.
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Human PRO polynucleotide #183.
US2003059909-A1.
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DB38657 standard; cDNA; 1857 BP. fovel human secreted and transmembrane protein PRO301 cDNA. IS2003082766-A1.
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MOVel human secreted and transmembrane protein PR0301 cDNA.
US200308269-A1.

01-MAY-2003.

(GETH ) GENENTECH INC.

Inc. Similarity: 100.00% Mismatches: 0

Match: 100.00% Indels: 0
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M92342 standard, cDNA; 1857 BP.
LOVel human secreted and transmembrane protein PRO301 cDNA.
152003082712-A1.
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Human PRO polynucleotide #183.
US2003082698-A1.
01-WAY-2003.
(GETH ) GENENTECH INC.
Sent Similarity: 100.00$
C Local Similarity: 100.00$
Ty Match: 100.00$
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Human PRO polynucleotide #183.
US2003082762-Al.
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                                                                                                                                                                                       DB15405 standard; cDNA; 1857 ... tuman PRO polynucleotide #183. fs2003087352-A1.
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(GETH) GENERATECH INC.
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(GETH) GENENTECH INC.
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(GETH) GENENTECH INC.
ent Similarity: 100.00%
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Query Match: 100.00 RESULT 131 ID ADB35034 standard; CDNA; DE Human PRO polynuclectide PN US2003077718-A1. PD 24-APR-2003. PPA (GETH ) GENENTECH INC.	Percent Similarity: 100.00# Percent Similarity: 100.00# M Query Match: 132 100.00# IN M DB36138 standard; cDNA; 1857 BP. DE Human PRO POlynucleotide SEQ ID NO PP 24-APR-2003 PAR-2001 PAR-201	ccent Similar it Local S sry Match: ULT 133 ADB4653. Novel hu US200300	Percent Similarity: 100.00\$  Percent Similarity: 100.00\$  Best Local Similarity: 100.00\$  Query Match: 100.00\$  RESULT 134  ID ADC26426 standard; cDNA; 1857 BP.  DE Human secreted/transmembrane protein PN US200369972-A1.	PA (GETH ) GENENTECH INC. Percent Similarity: 100.00\$ Cor Best Local Similarity: 100.00\$ Mis Best Local Similarity: 100.00\$ Inc RESULT 135 ID ADC39626 standard; CDNA; 1857 BP. DB Human secreted/transmembrane protein PN US2003059828-Al.	PD 27-MAR-2003. PPA (GETH ) GENETIECH INC. Percent Similarity: 100.00\$ Best Local Similarity: 100.00\$ Mis Query March: 100.00\$ RESULT 136 ID ADC40140 standard; cDNA; 1857 BP. DB Human secreted/transmembrane protein PN US20030598929-A1.	PA (GETH ) GENENTECH INC. Percent Similarity: 100.00\$ Mis Best Local Similarity: 100.00\$ Mis Query Match: 100.00\$ Ind RESULT 137  ID ADC18968 standard; CDNA; 1857 BP. DE Human secreted/transmembrane protein PD 20.FEB-2003:	PA (GETH ) GENENTECH INC. Percent Similarity: 100.00\$ Counter Match: 100.00\$ RESULT 138 RESULT 138 RESULT 138 DE Human secreted/transmembrane protein PN US200336094-A1. PD 20-FEB-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 100.00\$ Mis Query Match: 100.00\$ Mis Mis Mis Mis Mis Mis Mis Mis Mis Match: 100.00\$ Mis Match: 100.00\$ Mis Match: 100.00\$ Mis Mis Mis Mis Mis Mis Mis Mis Mis Match: 100.00\$
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Best Local Similarity: Query Match: RESULT 123 ID ADB39490 standard; DE Novel human secret: PN US2003082764-A1. PD 01-MAY-2003. PA (GETH) GENERICH	rce at ery Sul	15 to	it ce	PD 01-MAY-2003.  PA (GETH) GENENTECH INC Percent Similarity: 10 Best Local Similarity: 10 Query Match: 10 RESULT 127 ID ADB77325 standard; CD DE Novel human secreted	PN US2003082696-A1. PD 01-MAY-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 100.00 Guery Match: 100.00 Guery Match: 100.00 ESSULT 128 ID ADB34482 standard; CDNA; DE Human PRO polynucleotide PN US200307777-A1.	rce st sury	SUT SUT

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Novel human secreted and transmembrane protein PRO301 cDNA. US2003092106-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003092107-A1.
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Mismatches:
                         ADC29319 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
US2003049676-A1.
(GETH ) GENENTECH INC.
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RESULT 143

ID ADC33840 standard; CDNA; 1857 BP.
DE Human secreted/transmembrane protein CDNA, #25.
PN US2003073077-A1.
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US2003049677-A1.
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Human secreted/transmembrane protein cDNA, #25
US2003054400-Al.
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US2003054441-A1.
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Human secreted/transmembrane protein cDNA, #25.
US2003073079-A1.
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                     ID ADC29319 standard, c...., DE Human secreted/transmembrane properties of the prope
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PD 15-MAY-2003.
PA (GETH ) GENENTECH INC. Percent Similarity: 100.00% Best Local Similarity: 100.00%
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PD 20-MRR-2003.
PA (GETH) GENENTECH INC.
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PA (GETH ) GENENTECH INC.
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PD 17-APR-2003.
PA (GETH) GENENTECH IN Percent Similarity:
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PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH IN
Percent Similarity:
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RESULT 140
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RESULT 147
RESULT 139
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ADC57293 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein cDNA Seq ID365.
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RESULT 153

RESULT 153

DADG54584 standard; CDNA; 1857 BP.
DB Novel human secreted and transmembrane protein cDNA Seq ID365.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH') GRINGTHECH INC.
PA (GETH') GRINGTHECH INC.
Mismatches:
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PD US2003087365-A1.

PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.

Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query March: 100.00% Indels: 0
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Novel human secreted and transmembrane protein cDNA Seg ID365.
US2003087364-Al.
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ID ADCS0959 standard, cDNA, 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003087361-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA. US2003087367-A1.
08-MXY-2003.
  ADC59932 standard, cDNA, 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003092105-A1.
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RESULT 148
Th ADC52939 standard; cDNA; 1857 BP.
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ADC59068 standard; cDNA; 1857 BP
ID ADC59932 standard, ....., ENOVEL human secreted and trans BN US200302105-A1.
PD 15-MAY-2003.
PA (GETH ) GENEWIECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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(GETH ) GENENTECH INC.

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US2003087362-A1.
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16-OCT-2003.
(GETH ) GENENTECH INC.
    US2003194776-A1.
                                                                                                                          ADC55946 standard; cDNA; 1857 BP.

Novel human secreted and transmembrane protein cDNA Seq ID365.
US2003087360-A1.

(GB-MAY-2003.

(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                     ADC58516 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein cDNA Seq ID365.
US2003087346-A1.
 Novel human secreted and transmembrane protein cDNA Seg ID365.
US2003087359-A1.
08-MAY-2003.
(GETH ) GENENTECH INC.
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Wovel human secreted and transmembrane protein PRO301 cDNA. US2003092104-A1.
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Novel human secreted and transmembrane protein PRO301 CDNA.
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CDNA encoding human PRO polypeptide #183.

US2003194770-A1.
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Human PRO polynucleotide #183.
US2003194773-A1.
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Human PRO polynucleotide #183.
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DE Novel human secreted PN US2003087359-A1. PD 08-MAY-2003. PA (GETH) GENERET IP Percent Similarity: 18est Local Similarity: 10 Query Match:
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RESULT 157
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ADD04594 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003087354-A1.
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ID ADC80550 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003092103-A1.
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Human secreted/transmembrane protein cDNA, #25
US2003104469-A1.
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Human PRO polynucleotide #183.
US2003194771-A1.
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Human PRO polynucleotide #183.
US2003194774-A1.
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PA (GETH) GENENTECH INC.
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INC. 100.00% 100.00% 100.00%	cDNA; 1857 BP ectide #183.	100.00% 100.00% ; cDNA; 1857 BP	INC. 100.00% 100.00%	cDNA; 1857 BP nsmembrane pro	INC. 100.00% 100.00% 100.00%	cDNA;	INC. 100.00\$ 100.00\$	cDNA; 1857 BP n PRO polypept:	INC. 100.00% 100.00% 100.00%	cDNA, 1857 BP. n PRO polypeptide #183	INC. 100.00\$ 100.00\$ 100.00\$		INC. 100.008 100.008	cDNA; 1857 BP nsmembrane PRO
PD 0-2-UON-2-UOS. PA (GETH) GENERTECH Percent Similarity: Best Local Similarity: Query Match: RESULT 172	ID ADD09467 standard; cDNA; DE Human PRO polynucleotide PN US2003194775-A1. PD 16-OCT-2003. PA (GETH ) GRNENTECH INC. Percent Similarity: 100.00	Best Local Similarity: 100.00\$ Mismatch Query Match: 100.00\$ Indels: RESULT 173 ID ADD03923 standard; CDNA; 1857 BP. DE Human serreted/transmembrane profesor ONA.	PD US2003104381-71. PD 05-JUN-2003. PA (GETH) GENENTECH I Percent Similarity: Best Local Similarity: Decury Match:	ID ADD03499 standard; cDNA; 1857 BP. DE Human secreted/transmembrane protein cDNA, PN US2003108983-A1.	PD 12-JUN-2003.  PA (GETH) GENENTECH IP PERCENT SIMILARILY: BEST LOCAL SIMILARILY: COURTY MATCH:	AESOLI 173 ID ADD41180 standard; C DE Novel human secreted DN 115200320348-11	GOO3. GENENTECH Carity: milarity:	RESULT 176 ID ADD52319 standard; CDNA; 1857 BP. DE CDNA encoding human PRO polypeptide #18 PN US2003194769-A1. PD 16-OCT-2003.	PA (GETH ) GENENTECH INC. Percent Similarity: 100.00\$ Best Local Similarity: 100.00\$ Query Match: 100.00\$	ID ADD53059 standard; CDE CDNA encoding human US2003194792-A1.	PD 15-CL-2003. PD 46-CHT GENENTECH Percent Similarity: Best Local Similarity: Best Local Similarity: Best match:	ID ADD53611 standard; cDNA; DE Novel human secreted and PN US2003203437-A1. PD 30-OCT-2003.	(GETH ) GENENTECH cent Similarity: it Local Similarity: sry March:	TD AD37095 standard; cDNA; 1857 BP. DE Human secreted/transmembrane PRO polypeptide PN US2003105012-A1.

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ADE22306 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
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US2003194779-A1.
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1D ADD92499 standard; CDNA; 1857 BP. DE Human PRO polynucleotide #183.

PN US2003199030-A1.

PA (CETH ) GENEVTECH INC.

Percent Similarity: 100.00% M Query Match: 1857 BP. 100.00% M Guery Match: 1857 BP. 100.00%

RESULT 185

ID ADD91395 standard; CDNA; 1857 BP. DE Human PRO polynucleotide #183.
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PD 16-OCT-2003.

PA (GETH) GENENTECH INC.

Percent Similarity: 100.00%

Query Match: 100.00%

Query Match: 100.00%

RESULT 181

ID ADD02566 standard; cDNA; 1857 BP.

DE Human PRO polynucleotide #183.

PN US2003203431-Al.

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ADE04009 standard; CDNA; 1857
Human PRO polynucleotide #183.
US2003199057-A1.
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DE Human PRO polynuclectide #183
D 23-OCT-2003.
PA (GETH) GENENTECH INC.
PACCENT Similarity: 100.00$
Best Local Similarity: 100.00$
RESULT 186
ID ADD64009 standard; cDNA; 1857
DE Human PRO polynuclectide #183
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00$
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PA (GETH ) GENENTECH INC.
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Best Local Similarity: 100.00%
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RESULT 180
ID ADD51767 standard; cDNA; 1857
DE CDNA encoding human PRO polyg
PD US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
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15.7 Bl .ypept	AD79462 standard; CDNA; 1857 BP.  CDNA encoding human PRO polypeptide #183.  US2003203428-A1. 30.0CT-2003.  (GETH ) GENENTECH INC.  CDNSErvative:	0.0		DE Human PRO polymun PRO polymun PRO polymun PRO 199025-Al. PD 23-OCT-2003. PA (GETH ) GENENTEC Percent Similarity:
Cocal Similarity: 100.00\$  Match: 100.00\$  Match: 100.00\$  Match: 100.00\$  Match: 1857 BP  Mach PRO polynucleotide #183.  US2003194772-A1.  16-OCT-2003.  nt Similarity: 100.00\$		50 0		Querry Match: RESULT 198 ID ADE34751 standar DE Human secreted/k PN US-2003077583-A1. PD 24-APR-2003. PA (GTH ) GENENTE PERCENT SIMILATITY: Best Local Similarity:
Best Local Similarity: 100.00\$  Query Match: 100.00\$  RESULT 191  ID ADE17815 standard; CDNA; 1857 BP  BY US2003199023-A1.  PD 23-0CT-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 100.00\$  Best Local Similarity: 100.00\$  Query Match: 100.00\$	Mismatches: Indels: P. Conservative: Mismatches: Indels:	00 000		Query Match: RESULT 199 ID ADE18919 standar IDE Human PRO polynn PN US2003199026-A1. PD 23-OCT-2003. PA (CETH) GENENTE Percent Similarity: Rest Local Similarity Query Match: RESULT 200
T 192  ADD91947 standard; CDNA; 1857 BP Manan PRO polynucleotide #183. US2003199053.Al. 23-OCT-2003. int Similarity; 100.00% Local Similarity; 100.00% MATCh: MATCh:	•		•	ID AD543115 standax DE Human PRO polynu PN US2003199033-A1. PD 23-OCT-2003. PA (GETH ) GENENTEC Percent Similarity: Best Local Similarity; Query Match: RESULT 201
cDNA; 1857 BP ed and transme INC. 100.00%	transmembrane protein PRO301  Conservative: 0  Mismatches: 0	0301 cDNA.		DE HUMBAD PRO POLYMUM PRO POLYMUM PN US2003199059-A1. PD 23-OCT-2003. PA (GETH) GENENTEC Percent Similarity: Best Local Similarity Ouery Match:
7 BI	Match: Indels: 100.00\$ Indels: Transcript 100.00\$ Match: Transcript 100.00\$ Match: ADE33962 standard; cDNA; 1857 BP. Novel human secreted and transmembrane protein PR US2003194791-A1. 16-OCT-2003. (GETH ) GENENTECH INC.	PRO301 CDNA.		RESULT 202 ID ADE22790 standar DE CDNA encoding hu PN US203199064-A1. PD 23-OCT-2003 DA (GETH ) GENENTEC
7 Bi	nt Similarity: 100.00\$ Mismatches: Local Similarity: 100.00\$ Mismatches: Match: 100.00\$ Indels: T 195 Indels: ADB80014 standard; cDNA; 1857 BP. US2003207417-A1. 0G-NOV-2003. (GETH ) GENENTECH INC. nt Similarity: 100.00\$ Conservative:	oo o	٠.	Best Local Similarity Query Match: RESULT 203 ID ADD78908 standar DE CDNA encoding PN US2003203429-A1. PD 30-OCT-2003. PA (GEH) GENENTEC PERCENT Similarity: Best Local Similarity

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RESULT 212  ID ADG21156 stan DE Novel human s PN US2003207384- PD 06-NOV-2003.	Percent Similarity Best Local Similar Query Match: RESULT 213 ID ADF97491 stan DE Human PRO pol PN US20030730-	PA (GETH ) GRNEN Percent Similarity Best Local Similar Query Match: RESULT 214 ID ADG80555 stan DE Human PRO pol	PA (GETH ) GENENO Percent Similarity Best Local Similar Query Match: RESULT 215 ID ADG80003 stan DE Human PRO pol PN US2003207372-	5 # # #	5 # # B	2 t t E	DE Novel human s PN US2003207381- PD 06-NOV-2003. PA (GETH ) GENEN PERCENT SIMILATILY BEST LOCAL SIMILATILY BEST LOCAL SIMILATILY RESULT 219	DE NOVEL Human SENT CONTROL NOVEL Human SPN US2003207379-PD 06-NOV-2003.  PA (GETH ) GENEN Percent Similarity Best Local Similarity Query Match:  RESULT 220
0 PRO301 cDNA.	000 			<b>000</b>				PRO301 CDNA.: 0
la Indels: 1857 BP. transmembrane protein	Conservative Mismatches: Indels:	Conservative Mismatches: Indels: de #183.	Conservative Mismatches: Indels:	Conservative Mismatches: Indels:	Conservative Mismatches: Indels:	Conservative Mismatches: Indels:	Conservative Mismatches: Indels:	transmembrane protein PRO301 transmembrane protein PRO301  Conservative: 0 Mismatches: 0 Indels: 0
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Query Match: 100.00% RESULT 204 ID ADE32858 standard; cDNA; 1 DE Novel human secreted and t PN US2003194766-A1.	PA (GETH) GENENTECH INC. Percent Similarity: 100.00% Best Local Similarity: 100.00% Query Match: 100.00% RESULT 205 ID ADB42550 standard; cDNA; 1857 BI DE Human PRO polynucleotide #183. PN US2003199032-A1.	PD 23-OCT-2003.  PA (GETH ) GENENTECH INC.  PErcent Similarity: 100.00\$ Conser  Best Local Similarity: 100.00\$ Mismat.  Query Match: 100.00\$ Indels  RESULT 206  DE ADD80566 standard; CDNA; 1857 BP.  DE CDNA encoding human PRO polypeptide #183	0 t 8 E	PN US2003199028-Ā1. PD 23-OCT-2003. PA (GETH ) GENENTECH INC. Best Local Similarity: 100 Query Match: 100 RESULT 208 RESULT 208 LD ADB40878 standard; CDM DE Human PRO polynucleoti	PN US2003199031-A1. PD 23-OCT-2003. PA (GETH) GENENTECH INC. Percent Similarity: 100.00% Query March: 100.00% RESULT 209 ID ADB04677 standard; CDNA; 18	DE Human PRO polynucleotide #183. PN US2003199034-A1. PD 23-OCT-2003. PA (GETH) GENENTECH INC. Percent Similarity: 100.00% Guery Match: 100.00%	D   ADE92806 standard; CDNA; 1857 BP.	s standard uman secre 07355-A1. 2003. GENENTECH larity: imilarity:

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cDNA encoding human PRO polypeptide #21.
                US2002192659-A1.
                                                                                                                                              RESULT 211

ID AD164066 standard; CDNA; 1857 BP.

DE Novel human secreted and transmembrane protein PR0301 CDNA.

PN US2003207385-A1.

PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.

Percent Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207387-A1.
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US2003207377-A1.
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Novel human secreted and transmembrane protein PRO301 CDNA.
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US2003207386-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA.
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US2003054352-A1.
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ACA58390 standard; cDNA; 1857 BP
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                                   Human PRO polynucleotide #21
US2002146709-A1.
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PN US2003054352-A1.
PD 20-MAR-2003.
PA (GERH ) GENEWTECH IN
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ACU42376 standard; CDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 CDNA.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003087355-A1.
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Novel human secreted and transmembrane protein
US2003087353-A1.
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PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
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PA (GETH) GENENTECH INC.

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ID ADN16573 standard;
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RESULT 233
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PD 10 PA (G Percent Percent Best Lo Query M RESULT ID AD	DE HU PN US PD 29	PA (G Percent Best Lo Query M RESULT	ID AD DE CD	PA (G Percent Best Lo Query M RESULT	DE CD PN US PD 15	Percent Beat Lo Query M RESULT	DE ODE ODE ODE ODE ODE ODE ODE ODE ODE O	PA (G. Percent Best Lo Query M RESULT		ត្ត ក អូទ្	DE Hu PN US	PA (G Percent Best Lo Query M RESULT	DE BUNG	합 한 것 같	DE HU DE HU PN US
000	PRO301 cDNA.	000		000		000		000		000		000		000	
Conservative: Mismatches: Indels:	protein	Conservative: Mismatches: Indels:	ein cDNA, #25.	Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:	ein cDNA, #25.	Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:	in cDNA, #25.
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PN US2003087357-A1. PD 08-MAY-2003. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	ADC81102 standard; cDNA; 1857 BP. Novel human secreted and transmembrane US2003092115-Al.	PD 15-MAY-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 100.00%  Best Local Similarity: 100.00%  Query Match:	T 238  BDT99196 standard; CDNA; 1857 BP.  Human secreted/Fransmembrane protein CDNA, 122093135025-Al.	ENTECH ty: arity:	AD76550 standard; cDNA; Human PRO polynucleotide US2003100087-A1. 29-MAY-2003.	PA (GETH ) GENENTECH INC. Percent Similarity: 100.00* Best Local Similarity: 100.00\$ Query Match: 100.00\$	KESULI 290 ID ADD8791 standard; CDNA; 10 DE Human PRO polynucleotide #: PN US2003092113-A1.	PA (GETH ) GENERATECH : Percent Similarity: Best Local Similarity: Query Match:	DD86318 standard; uman PRO polynucl S200320340-A1.	PD 30-007-2203. PA (GETH) GENENTECH INC. Percent Similarity: 100.00% Best Local Similarity: 100.00% Query Match: 100.00%	ADE79620 standard; cDNA; 1857 BP. Human secreted/transmembrane protein cDNA, US2003130489-A1.	PP 10-JUL-2003. PA (GETH) GENENTECH INC. Percent Similarity: 100 Best Local Similarity: 100 Query Match: 100	6 standard; RO polynucl 11571-Al.	Z003. GENENTECH larity: imilarity:	7.427296 standard; cDNA; 1857 BP. Human secreted/transmembrane protein cDNA, US2003129592-A1.
PN US200 PD 08-MA PA (GETH Percent Si Best Local Query Matc RESULT 237	DE DE C	PD 1 PA ( Percen Best L	RESULT ID A DE H	PA (PERCEN PERCEN DOMENT)	PN P	PA (Percen Best L Query	DE D	PA (Percen Best L Query	ID PN	PD 3 PA ( Percen Best L Query D	DE H	PD 10-JUL- PA (GETH) Percent Simi Best Local S Query Match:	PN	PD 13-NOV- PA (GETH) Percent Simi Best Local S Query Match:	ID AI ID AI DE HI

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UB41303 standard; cDNA; 1857 BP.
Uman secreted/transmembrane PRO polypeptide cDNA #27.
182003100497-A1.
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ADE73831 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
US2001148370-A1.
07-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                    DE23894 standard; cDNA; 1857 BP.
DNA encoding human PRO polypeptide #183.
S2003092110-A1.
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DNA encoding human PRO polypeptide #183.
S2003092111-A1.
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S2003092108-A1.
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BEB9228 standard; cDNA; 1857 BP.
Luman PRO polynuclectide #183.
IS2003199062-A1.
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(GETH ) GENENTECH INC.
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PA (GETH ) GENENTECH I Percent Similarity: Best Local Similarity: Query Match: RESULT 253 ID ADE18367 standard; DE Human PRO polynucle PN US2003194794-A1. PD 16-OCT-2003. PA (GETH ) GENENTECH II		PA (SETH) GENENTECH INC. Percent Similarity: 100.00\$ Best Local Similarity: 100.00\$ Mis Query Match: 100.00\$ RESULT 255 ID ADE99385 standard; cDNA; 1857 BP. DE Human secreted/transmembrane protein	g # 7 g	ID ADE94696 standard; ID CONA, ID CONA, ENA, encoding human PRO pop NV US2003199027-A1.  PD 23-OCT-2003.  PA (GETH) GENENTECH INC. Percent Similarity: 100.00% Best Local Similarity: 100.00% RESULT 257  ID ADE91107 standard; CDNA, ID HUMAN PRO DOLYMUClectide # NV US2003199061-A1.	PA (GETH ) GENENTECH INC Percent Similarity: 10 Best Local Similarity: 10 Query Match: 10 RESULT 258 ID AB95248 standard; CD DE CDNA encoding human P PD 23-OCT-2003.	GENENTECH arity: milarity: standard, O polynuc] 9060-A1.	PA (GETH ) GENENTECH INC Percent Similarity: 10 Query Match: 10 RESULT 260 ID ADF34939 standard; cD DC CDNA encoding human P PN US2003199029-A1. PD 23-OCT-2003. PA (GETH ) GENENTECH INC

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rcent Similaritest Local Simils est Local Simils est Match: 261. SULT 261. ADE98504 8tt Human secret US2003211565 13-NOV-2003 (GETH ) GENT CEENT SIMILARITE ET MATCH: SULT 262 SULT 262 MATCH: 162 MATCH: 163 MATCH: 164 MATCH: 165 MAT	Novel human secret US2003199051-A1. 23-0CT-2003. (GETH) GENENTECH rcent Similarity: st Local Similarity: sty Match: SULT 263 ADE90555 standard; Human PRO polynuci US2003199063-A1. 23-OCT-2003. (GETH) GENENTECH	roent Similarity: at Local Similarity: ary Match: sry Match: NOVel Numan Secret US2003199058-AI.	(GETH ) GENENTECH CECHT Similarity: ST Local Similarity: ST Match: SULT 265 Human secreted/tre US2003211568-A1. 13-NOV-2003.		Percent Similarity: Best Local Similarity: Best Local Similarity: Busy Match: EESULT 267  ID ADP73795 standard; DE Human secreted/tra PN US201380312-A1. PD 25-SEP-2003. PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: RESULT 268
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cDNA encoding human PRO polypeptide #183.

US2003207359-A1.

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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207360-A1.
06-NOV-2003.
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Novel human secreted and transmembrane protein PRO301 CDNA.
US2003207426-A1.
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CDNA encoding human PRO polypeptide #183.
US2003207376-A1.

06-NOV-2003.

(GETH ) GENENTECH INC.
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st Local Similarity: 100.00$ Indels:
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ID ADG02281 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% MESUL Cocal Similarity: 100.00% IRESULT 269
ID ADG22067 standard; cDNA; 1857 BP.
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US2003207351-Al.
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US2003207353-A1.
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ADG16751 standard; cDNA; 1857 BP.
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PA (GETH) GENENTECH INC.
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DE Novel human secreted and transmembrane protein length of the constant of the constant
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cDNA encoding human PRO polypeptide #183.
US2003207425-Al.
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cDNA encoding human PRO polypeptide #183.
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cDNA encoding human PRO polypeptide #183.
US2003219885-A1.
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Human PRO polynucleotide #183.
US2003207371-A1.
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Human PRO polynucleotide #183.
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RESULT 284
ID ADG06124 standard;
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RESULT 298
                                                                                              AUG23708 standard; CDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 CDNA.
US2003207389-A1.
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DE Novel human secreted and transmembrane protein PRO301 cDNA.

PN US2003207427-A1.

PA (GETH ) GENRUTECH INC.

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RESULT 292

ID ADG62010 standard; cDNA; 1857 BP.

DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207428-A1.
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Novel human secreted and transmembrane protein PR0301 cDNA.
06-NOV-2003.
(GETH.) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO301 CDNA.
US20032073356-Al.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207390-Al.
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052003207423-A1.
                                                                                                                   DE NO.

PN US200320730.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Percent Similarity: 100.00$

Best Local Similarity: 100.00$

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PA (GETH ) GENENTECH INC.

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RESULT 291
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Query Match:
RESULT 295
ID ADG57450 standard; cDNA; 1857 BP.
DE NOVel human secreted and transmembrane protein PRO301 cDNA.
DN US2003207362-A1.
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Novel human secreted and transmembrane protein PRO301
US2003207368-A1.
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ADG56898 man secreted and transmembrane protein US2003207364-A1.
                                                                       Human secreted/transmembrane protein cDNA, #25.
US2003027145-Al
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Human secreted/transmembrane protein cDNA, #25:
052003027146-A1.
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                                                          CDNA; 1857
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US2003207358-A1.
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PD 06-NOV-2003.
PD (GETH) GENENTECH INC.
Percent Similarity: 100.00%
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RESULT 294
Th ADG82211 standard; c
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                                                          ADG92214 standard;
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RESULT 309 ID ADG54138 stand DE NOVG1 human se PN US2003207416-7 PD 06-NOV-2003. PA (GETH ) GENENT Percent Similarity; Best Local Similarity RESULT 310 ID ADG81107 stand PE Human PRO POLY PN US2003194793-7 PD 16-OCT-2003	Surv Surv	PA (GETH ) GENENT Percent Similarity Best Local Similarity Query Match: RESULT 312 ID ADH12612 stand DE NOVEL human se PN US2003207378-7 PD 06-NOV-2003. PA (GETH ) GENENT Percent Similarity.	Best Local Similari Query Match: RESULT 313 ID ADG61458 stanc DE Novel human se PN US2003207429-7 PD 06-NOV-2003. PA (GETH) GENENY Percent Similarity?	Best Local Similari Guery March: RESULT 314 ID ADH28545 stand DE Human PRO poly PN US2003022331-7 PD 30-JAN-2003.	Petrent Similarity Best Local Similarity Query Match: RESULT 315 ID ADG54690 stanc DE Novel human se PN US2003207367-7	rcent Simil st Local Si sary Match: SULT 316 MOVEL NOVEL HU US200320 06-NOV-2 (GETH ) rcent Simil
301 CDNA.		·		ΑΝ.	301 CDNA.	301 cDNA.
0% Mismatches: 0 Indels: 0	answembrane process Conservative: Mismatches: Indels: 57 BP.	Conservative: 0 Mismatches: 0 Indels: 0 357 BP.	O% Conservative: 0 O% Mismatches: 0 O% Indels: 0 1857 BP. #183.	Conservative: 0 Mismatches: 0 Indels: 0 357 BP.	O\$ Conservative: 0 O\$ Mismatches: 0 O\$ Indels: 0 1857 BP. transmembrane protein PRO301	Conservative: 0 Mismatches: 0 Mismatches: 0 Mismatches: 0 Mismatches: 0 Mismatches: 0 Cransmembrane protein PRO301
Best Local Similarity: 100.00% Ouery March: 100.00% ESULT 301 DD ADG58002 standard; CDNA; 18 DD NOVEL human serreted and tr PN US2003207363-A1. PA (GETH ) GENENTECH INC. PA (GETH ) GENENTECH INC. PRECORT Similarity: 100.00% Ouery March: 100.00% RESULT 302 RESULT 302 DD ADG53586 standard; CDNA; 18 DD NOVEL human secreted and tr	CH INC. 100.0 Y: 100.0 rd; cDNA; reted and	PN U52003207421-A1. PD 06-NOV-2003. PA (CETH) GENEWECH INC. Percent Similarity: 100.00% Query Match: 100.00% RESULT 304 ID ADG81659 standard; cDNA; 1857 BP DE Human PRO polynucleotide #183. PN 052003207805-A1.	100.0 100.0 100.0 ; cDNA; leotide INC.	Percent Similarity: 100.00\$ Best Local Similarity: 100.00\$ Guery Match: 100.00\$ ID ADG63620 standard; cDNA; 1857 BP DE Human secreted/transmembrane poly PD 25-SEP-2003.	Gambulach inc. 0 imilarity: 100.0 imilarity: 100.0 100.0 8 standard; CDNA; uman secreted and 07419-A1.	PA (GETH ) GENENTECH INC. Percent Similarity: 100.00\$ Best Local Similarity: 100.00\$ Query Match: 100.00\$ RESULT 306 ID ADG52410 standard; CDNA; 18 DE NOVel human secreted and tr PN US2003207414-A1. PD 06-NOV-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 100.00\$

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100.00%	ADH20430 standard; cDNA; 1857 BP. Human secreted/transmembrane protein US200405553-A1. (GETH) GENENTECH INC. stt Similarity: 100.00\$ Local Similarity: 100.00\$ Mis. Local Similarity: 100.00\$	standard; cDNA; 1857. O polynucleotide #27. 4984-A1. 003. GENENTECH INC. arity: 100.00%	d; cDNA; 185' ransmembrane S L. P J. P J. P M. 100.00\$	ADH55830 standard; cDNA; 1857 BP.  Human secreted/transmembrane protein cDNA, 20-NOV-2003.  (GETH ) GENENTECH INC.  (GETH ) GENENTECH INC.  Local Similarity: 100.00\$ Mismatch  MATCH:  MATCH:	SULT 321 ADH06858 standard; CDNA; 1857 BP. Human secreted/transmembrane protein cD US2004005665-A1. (D8-JAN-2004. (DESN/) DESNOYERS L. (GODD/) GODDARD A. (GODD/) GODDARD A. (GOND/) GUNEY P J. (GURN/) GUNEY A L. (MATH/) MATHER U P. (WILL/) WILLIAMS P M. (WILL/) WILLIAMS P M. (WOOD/) WOOD W I. roent Similarity: 100.00\$ Conse	100.00\$ d; cDNA; 1857 man PRO polyg 100.00\$ 100.00\$ 100.00\$ d; cDNA; 1857 ransmembrane
Query Match:	DE Human secreted/t PN US20400553-A1. PD 08-0AN-2004. PA (GETH ) GENENTEC Percent Similarity: Best Local Similarity: Query Match:		398830000088	10 ADM159830 standar DE Human secreted/t PN US2003215904-A1. PD 20-NOV-2003. PA (GETH ) GENENTEC Percent Similarity: Guery Match:	RESULT 321  D ADH06858 standard DE Human secreted/tr PN US2004005665-A1. PD 08-JAN-2004. PA (GDDD/) GDDBARD PA (GDDO/) GDDBARD PA (GDOV) GUNBER PA (GDV) GUNBER PA (GDV) GUNBER PA (WILL/) WILLIAMS PA (WILL/) WILLIAMS PA (WOOD/) WOOD W I.  Percent Similarity: Best Local Similarity:	Query Match: RESULT 322 ID AD181154 standar DE CDNA encoding hu PN US2003207361-A1. PN (GETH ) GENEYEC PECCEL Similarity: Best Local Similarity: Best Local Similarity: Cuery Match: RESULT 323 ID AD118600 standar DE Human secreted/t PN US200315299-A1. PD 14-AUG-2003. PA (GETH ) GENENTEC

Percent Simil Best Local Si Guert Match:  RESULT 31843  ID AD 1843  PD 07-AUGO-  PA (GETH)  PRESULT 3185  PD 07-AUGO-  PD	Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 100.00\$ Indels: 0	SULT 324 AD165320 standard; Human secreted/tra US2003148419-A1. 07-AUG-2003.	Social Simil Local Si	0	PD 2Z-MAY-2003.  PA (GETH) GENEVIECH INC. Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0	T C	PD 15-JAN-2004.  A (GETH) GENENTECH INC. Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0	OF THE	D 09-OCT-2003. A (GETH ) GENEVIECH INC. ercent Similarity: 100.00% Conservative: 0 est Local Similarity: 100.00% Mismatches: 0 uery Match: 00.00% Indels: 0	In a	0 >		[김윤취경호]	ESULT 330  AD165747 standard; cDNA, 1857 BP.  E Human secreted/transmembrane protein cDNA, #25.  N US2003148371-A1.	e tr	ESDLM 331 A AD114700 standard; cDNA; 1857 BP. E Novel human secreted and transmembrane protein PRO301 cDNA.	PN US2003207383-A1.
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Human PRO polynucleotide #183
US2004038336-A1.
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RESULT 341
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AD118295 standard; cDNA; 1857 BP.
UNCVE1 human secreted and transmembrane protein PRO301 cDNA.
US2003207449-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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US2003186358-A1.
02-OCT-2003.
                                                                                     ADH60490 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
US2004023331-A1.
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PN US2003187238-A1.
PN 02-007-2003.
PA (GETH.) GENENTECH INC.
Percent Similarity: 100.00% C
Best Local Similarity: 100.00% I
RESULT 335
ID ADL08740 standard; CDNA; 1857 BP.
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RESULT 334
ID ADJ99547 standard; cDNA; 1857 BP.
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RESULT 338
ID 338
SESULT 338
B US2031 standard; CDNA; 1857 BP.
DE Human secreted/transmembrane prot PD 09-0CT-2003.
PD 09-0CT-2003.
PA (GETH.) GENENTECH INC.
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ID ADM25081 standard; cDNA; 1857 BP.
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DE Human secreted/transmembrane IP US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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Percent Similarity: 100.00$
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PA (GETH ) GENENTECH INC.

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%
                                                                               DE ADHGO490 standard; cDNA, DE Human secreted/transmemth US2004023331-A1.

PA US2004023331-A1.

PA (GDDA) GODDARD A.

PA (GODD/) GODDARD A.

PA (GDDA) GODDARD A.

PA (GDRN/) GURNEY A L.

PA (GURN/) GURNEY A L.

PA (WILL/) MILLIAMS P M.

PA (WILL/) MILLIAMS P M.

PA (WILL/) MILLIAMS P M.

PA (WODD/) WOOD W I.

PECCENT SIMILATICY: 100.

QUELY MATCH:

RESULT 333.
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PD 26-FEB-2004.
PA (GETH) GENERTECH INC.
Percent Similarity: 100.
Best Local Similarity:
                             Query Match:
RESULT 332
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RESULT 343
ID ADM42453 standard; cDNA; 1857 BP.
DE CDNA encoding human PRO polypeptide #183.
PN US2004058424-Al.
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                                                                                                                                                                                                                                                                                                                                                                       CDNA encoding human PRO polypeptide #183.
                                                                                                                                                                                                                                          ADJ65593 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2004038335-A1.
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US2004077064-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
RESULT 344
ID ADO06153 standard, cDNA; 1857 BP.
DE Human PRO polynucleotide #23.
PN US686451-B1.
PN US686451-B1.
PA (GETH ) GENENTECH INC.
PARCHER SIMILARITY: 100.00$
Best Local Similarity: 100.00$
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ID ADRI7914 standard; CDNA; 1857 BP. DE Human secreted/transmembrane protein V US2004147017-Al. PA (ASHK/) ASHKENAZI A. PA (ASHK/) ASHKENAZI A. PA (BENZ/) BOTSTEIN D. PA (BRNZ/) BESROYERS L. PA (ERIK/) ERERRARA N. PA (FILV/) FILVAROFF E. PA (FILV/) FOUGS S.
                                                                                                  CDNA; 1857 BP
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                                                                                                                   Human PRO polynucleotide #27
US2004043927-A1.
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Best Local Similarity: 100.00$

100.00$
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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Percent Similarity: 100.00$
Best Local Similarity: 100.00$
Ouery March: 100.00$
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Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match:
                                                               Query Match...
RESULT 340
TD ADK82831 standard; C'
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GRIMALDI C J.

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ID AD196349 standard, cDNA, 1857 BP.

DE Novel human secreted and transmembrane protein PRO301 CDNA.

PN US2003207354-A1.

PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.

Percent Similarity: 100.00$ Conservative: 0

Best Local Similarity: 100.00$ Mismatches: 0

Query_Match: 100.00$ Indels:
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Mismatches:
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US2003152922-A1.
14-AUG-2003.
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Indels:
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CDNA encoding human PRO polypeptide #183.
US2003077659-A1.
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US2004185531-A1.
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RESULT 349
ID ADT03590 standard; cDNA; 1857 BP.
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Human PRO301 cDNA sequence.
AUZ003259607-A1.
27-NOV-2003.
(GETH ) GENENTECH INC.
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Local Similarity: 100.00%

Match: 100.00%
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PAONI N F.
ROY M A.
STEWART T A.
TUMAS D.
WILLIAMS P M.
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GODDARD A.
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DESNOYERS L.
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GODDARD A
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                               GODOWSKI
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(BOTS/)
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(GODO/)
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Human secreted protein-encoding gene 23 cDNA clone HACAA29, SEQ ID NO:33.
WO200136440-A1.
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WO200136440-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE07127 standard; DNA; 1943 BP.
Novel coding sequence (useful for identifying genetic disorders) #193.
WO2003054152-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR46572 standard, DNA; 2009 BP.
Human JAM-1, Fll receptor (FllR) transcript variant 4, encoding gene.
JP2004242513-A.
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Novel DNA-related contig nucleotide seguence #139.
WO2003054152-A2.
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Mismatches:
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Mismatches:
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Mismatches:
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Human cDNA encoding a novel human protein #275.
WO200155437-A2.
                                                                                                                                                                                                                                                                                                                                                               AAS22710 standard; cDNA; 1902 BP.
Human cDNA encoding a novel human protein #276.
WO200155437-A2.
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Indels:
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RESULT 356
ID AAD08335 standard; cDNA; 1918 BP.
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PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 100.00$
Best Local Similarity: 100.00$
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PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 100.00$
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PA (HYSE-) HYSEQ INC.
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                                                      PAN J.
PAONI N F.
ROY M A.
STEWART T A.
TUMAS D.
WILLIAMS P M.
GURNEY A L.
HILLAN K J.
KLJAVIN I J.
MATHER J P.
                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
RESULT 352
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Percent Similarity:
Best Local Similarity:
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Percent Similarity:
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Query Match:
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                                                                                                                                  (WILL/)
(WOOD/)
                                                                                                                     TUMA/)
                                                                                       ROYM/)
                            (KLJA/)
                                                                        (PAON/
                                                                                                     STEW/
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ADQ68025 standard; cDNA; 2141 BP.
Recombinant vector preparation human clone cDNA, PLACE1005544.
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PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Percent Similarity: 100.00% Conservative:
Best Local Similarity: 100.00% Mismatches:
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Mismatches:
Indels:
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PN W0200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PARCENT Similarity: 100.00% Conservative:
Best Local Similarity: 100.00% Mismatches:
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Mismatches:
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Mismatches:
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WO200160860-A2.
23-AUG-2001.
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                                                                                                                                                                                                                                                                    AAK94509 standard; cDNA; 2141 BP.
Human full-length cDNA, SEQ ID NO: 3364.
EP1130094-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                           ADL31331 standard; cDNA; 2141 BP.
Full length human cDNA clone SeqID 3364.
EP1396543-A2.
                                                                                                            ADL26799 standard; cDNA; 2100 BP.
Human JAMI encoding cDNA SEQ ID NO:53.
WO2004022778-A1.
                                                                      Query Match: 100.00$

RESULT 359

ID ADL26799 standard; cDNA; 2100 BP.

DE Human JAM1 encoding cDNA SEQ ID NO PN W02004022778-A1.

PD 18-MAR-2004.

PA (GARV-) GARVAN INST MEDICAL RES.

Percent Similarity: 100.00$

Beet Local Similarity: 100.00$

Query Match: 100.00$
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ABV22266 standard; cDNA; 3389 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                          DE Full length numan cons comment of the EP1396541-A2.

PD 10-MAR-2004.

PD 16-MAR-2004.

PD 16-MAR-2004.

Percent Similarity: 100.00%

Best Local Similarity: 100.00%
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ABV28103 standard; cDNA; 3389 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADN05139 standard; cDNA; 2187 BP.
Antipsoriatic cDNA sequence #785.
WO2004028479-A2.
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AAS22473 standard; cDNA; 2259 BP.
                                                                                                                                                                                                                                                                     ID AAK94509 standard; cDNA; 2141
DE Human full-length cDNA, SEQ 1
PD 05-SEP-2001.
PA (HELL-) HELIX RES INST.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
RESULT 361
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PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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PN W0200155437-A2.
PD 02-AUG-2001.
PA (HYSE) HYSEQ INC.
Percent Similarity: 1
Best Local Similarity: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DE Recombinant vector programmer of DP200421565-A. PD 05-AUG-2004.
PA (ZOIJ-) ZOIJIN KK. Percent Similarity: 18est Local Similarity: 1
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(GETH ) GENE
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RESULT 364
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ADR46576 standard; DNA; 3861 BP.
Human F11 receptor (F11R) transcript variant 4, encoding gene, SEQ ID
                                                                                                                                                                                                 encoding gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ61781 standard; cDNA; 1421 BP.
cDNA encoding human A33 receptor homologue, SEQ ID NO:254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding human A33 receptor homologue, SEQ ID NO:70.
WO9955865-A1.
                                                                                                                                                                                           Human JAM-1, F11 receptor (F11R) transcript variant 1, JP2004242513-A. 02-SEP-2004 (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
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Human JAM-1, Fl1 receptor (F11R) transcript variant
JP2004242513-A.
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PD 02-504.

PD 02-504.

PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH
Percent Similarity: 100.00% Conservative:
Best Local Similarity: 100.00% Mismacches:
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                          Conservative:
Mismatches:
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Human cDNa isolated from skin cells SEQ ID NO:
WO200190357-A1.
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PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 100.00% Conservat
Query Match: 100.00% Indels:
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ent Similarity: 99.67% C.
Local Similarity: 99.67% M
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(GENE-) GENESIS RES & DEV CORP LTD.
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                                                                                                                                                             DNA; 3660 BP.
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Skin cell cDNA, SEQ ID NO: 254.
WO200069884-A2.
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ID NO: 70.
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Best Local Similarity: 100.00$
Onerv Match: 100.00$
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Best Local Similarity: 100.00%
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Local Similarity: 99.67%
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                                                                                                                              RESULT 367
ID ADR46570 standard;
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RESULT 371
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0 70 0	o	070		707		0 1 53		0 0 181		3 12		23	0 23	
Conservative: Mismatches: Indels:	BP. cells SEQ ID NO: 7	LTD. Conservative: Mismatches: Indels:	nsus sequence.	Conservative: Mismatches: Indels:	ID NO:119.	Conservative: Mismatches: Indels:	ID NO:118.	Conservative: Mismatches: Indels:	; 924 BP. ule gene.	AG F. Conservative: Mismatches: Indels:	BP. CDNA SEQ ID NO 30.	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	120.
nnt Similarity: 99.33% Local Similarity: 99.33% Match: 99.22%	tandard; cDNA; 1421 isolated from skin 7-A1.	2001. GENESIS RES & DEV CORP larity: 99.33* imilarity: 99.23*	0 D 4 -	.Zo-rawlersysy. (GETH ) GENENTECH INC. int Similarity: 99.34% Local Similarity: 99.00% ' Match: 98.12%	TESOLI 37/ ID ADJ6/405 standard; DNA; 4249 BP. DE Human ovarian specific gene SEQ PN W02004013311-A2. DD 12-EPB-2004	FED-JUGS. Similarity: 84.66% cal Similarity: 84.66% tach: 96.31%	4 standard; DNA; 4633 BP. varian specific gene SEQ 13311-A2.	PA (DIAD-) DIADEXUS INC. Percent Similarity: 62.29\$ Best Local Similarity: 62.29\$ Query March: 92.36\$	AAV28136 standard; cDNA to mRNA; Human junctional adhesion molecul WO9824897-A1.	A ROCHE & CO 94.65% 93.65% 91.16%	; cDNA; 1812 lin encoding	S = 10.5	ABA06454 standard; cDNA; 1812 BP Human cDNA SEQ ID NO: 120. WC200154474-A2. 02-AUG-2001. HUMAA. PUWAN GENOME SCI INC. ent Similarity: 91.97% Local Similarity: 91.97% Match: 90.45%	ABV03791 standard; cDNA; 1812 BP Human polymucleotide SEQ ID NO 1 1202002090672-A1. (ROSE/) ROSEN C A. (ROSE/) RUBEN S M.
Percent Simi Best Local S Query Match:	5	3 t t	ID AA ID AA DE Hu PN WO	PA (G PA (G Percent Best Lo Query M	ID ADJ67405 ID ADJ67405 DE Human ov PN 12-EFB-21	PA (DIAD-) Percent Simi Best Local S Query Match:	ID AD	PA (DIAD-) PA (DIAD-) Percent Simi Best Local S Query Match: PESHT, 179	ID AA DE Hu	PD 11 PA (H) Percent Best Lo Query M,	ID AA	PD 02-AUG-2 PA (HUMA-) Percent Simil Best Local Si Query Match: RESULT 381	ID ABP DE Hun PN WOJ PD 02- PA (H Percent Best Loc Query ME	1D AB DE Hun PN US PD 11 PA (RC

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D ADR46574 standard; DNA; 3527 BP.

D ADR46574 standard; DNA; 3527 BP.

EN JP2004242513-A.

PN O2-SEP-2004.

PA (DOXU-) DOXUNITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.

Percent Similarity: 86.29$ Mismatches: 1

QUELY MATCh: 1387.

RESULT 387.
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DE Human CDNA clone representative sequence, SEQ ID NO: 1790.
DE Human CDNA clone representative sequence, SEQ ID NO: 1790.
DN EP130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 97.10% Mismatches: 7
Query Match: 78.50% Indels: 0
RESULT 389
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5' end of a representative human CDNA cluster SeqID 1790.
EP1396543-A2.
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Human CD-like molecule HKACI03 cDNA, SEQ ID NO:145.
WO200226930-A2.
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Mismatches:
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                                                                                                                                                ADB31509 standard; cDNA; 1812 BP.
Human cDNA encoding a novel protein SEQ ID NO
US2003077606-A1.
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Indels:
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Human cDNA encoding a novel human protein #40
WO200155437-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID ADQ95891 standard; CDNA; 1116 BP.

DE T cell activation associated CDNA #35.

PN WGO00405805-A2.

PD 15-JUL-2004.

PA (ASAH-) ASAHI KASEI PHARMA CORP.

Percent Similarity: 86.29* Mismatch Conery Best Local Similarity: 86.29* Indels: RESULT 386

DE Human JAM-1, F11 receptor (F11R) transcrip N JP2004242513-A.

PA 02-SEP-2004.

PA (OSUY-) DOKURITSU GYOSEI HOJIN KAGAKU GIJD PROCESSI FOR THE PARTY AND THE P
                                                                                                                                    ID ADDA --
DE Human CDNA e...

PN US2003077666-A1.

PD 24-PR-2003.

PA (HUMA-) HUMAN GENOME SCI INC.

Percent Similarity: 91.97%

Beet Local Similarity: 91.97%

"atch:
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(REAS-) RES ASSOC BIOTECHNOLOGY.
ent Similarity: 97.10%
Local Similarity: 97.10%
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F11 antigen coding sequence.
W09902561-A1.
21-7AN-1999.
(SMIK ) SMITHKLINE BEECHAM CORP.
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(HUMA-) HUMAN GENOME SCI INC.
ent Similarity: 91.97%
Local Similarity: 91.97%
                              91.97$ 91.97$
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85.95%
82.97%
PA (BARA/) BARASH S C.
Percent Similarity: 91
Best Local Similarity: 91
Query Match: 99
RESULT 383
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DE Human CD-11ke molecu
PN WO20022630-A2.
PD 04-ARR-2002.
PA (HUMA-) HUMAN GENOME
Percent Similarity: 9
Query Match: 99
RESULT 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID AAS22474 standard; cl
DE Human CDNA encoding -
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE) HYSEQ INC.
Percent Similarity: 8
Best Local Similarity: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
RESULT 388
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ADH62531 standard; DNA; 726 BP.

Human consen01 DNA used to isolate DNA40628 encoding PRO301 protein.
US2003171568-A1.

[1.-SEP-2003.

(ASHK.) ASHKENAZI A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse junctional adhesion molecule-1 encoding gene, SEQ ID 11.
JP2004242513-A.
02-SEP-2004.
                                                                                                                                                                                                                                                                        ABX93346 standard; cDNA; 726 BP.
Consensus sequence expressed sequence tag, EST, consen01.
US2002182206-A1.
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3 4 9
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Percent Similarity: 83.06% Conservative:
Best Local Similarity: 68.44% Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
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PA (HOFF) HOPFMANN LA ROCHE & CO AG F.

Conservative:

Best Local Similarity: 68.11% Mismacches:

A 531% Indels:
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Mismatches:
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Mismatches:
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Mismatches:
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Mismatches:
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Mismatches:
                                                                                                                       Nucleotide sequence used to isolate DNA40628 WO9927098-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
RESULT 399
RESULT 390
ADN35287 standard; DNA; 726 BP.
DE Human PRO301 DNA fragment consens01.
PN WO2004031105-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV88991 standard; cDNA; 612 BP.
EST clone IJ638.
WO9845437-A2.
                                                                                                           AAX81767 standard; DNA; 726 BP
                                                                                                                                                                                                                                                                                                            US200zicz.
05-DEC-2002.
(GETH ) GENENTECH INC.
rcent Similarity: 99.07%
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PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 99.07%
Best Local Similarity: 98.60%
                                                                                                                                                       PN 03-JUN-1999.
PD 03-JUN-1999.
PA (GETH ) GENENTECH INC.
Percent Similarity: 99.07%
Best Local Similarity: 70.01%
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68.44%
69.92%
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70.01%
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(GEMY) GENETICS INST INC.
ent Similarity: 99.49%
Local Similarity: 99.49%
 PD 14-AUG-2003.

PA (GENE-) GENE LOGIC INC.

Percent Similarity: 82.7

Best Local Similarity: 71.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GURN/) GURNEY A L.
(NAPI/) NAPIER M A.
(TUMA/) TUMAS D.
(WOOD/) WOOD W I.
                                                                                                                                                                                                                                                                                                                                                PA (GETH / CALL)
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FONG S.
GODDARD A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
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RESULT 396
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RESULT 400
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RESULT 402
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RESULT 397
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RESULT 401
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Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4051.
WO2003065993-A2.
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Mismatches:
Indels:
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Mismatches:
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Indels:
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Indels:
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Human polynucleotide SEQ ID NO 94
US2002090672-Al.
                                                                       ABA06428 standard; cDNA; 1894 BP.
Human cDNA SEQ ID NO: 94.
WO200154474-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ACA10115 standard; cDNA; 750 BP. Human NOVX polynucleotide #5. WO200290504-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                       ID ABA06428 standard; cDNA; 1894 BDE Human cDNA SEQ ID NO: 94.
PN WO20015474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 85.71%
Best Local Similarity: 75.75%
Query Match:
RESULT 392
                                                                                                                                                                                                                                    ID ABV83765 stanuald, C...,

BE Human polynucleotide SEQ ID N
US2002090672-A1.

PD 11-UUL-2002.

PA (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.

Percent Similarity: 85.71%

Best Local Similarity: 75.75%
                                                                                                                                                                                                                                                                                                                                                                                                                                       D ACA10115 standard; c....,
DE Human NOVX polynucleotide #5
PN WC200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 75.25#
Best Local Similarity: 75.25#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AD008262 standard; cDNA; 750
Human NOVX polynucleotide #5.
US2004018594-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID AD008262 standard, cDNA, 75G
B Human NOVX polynuclectide #5D
B (US2004018594-A1.)
PD 29-JAN-2004.
PA (ALSO)/ ALSOBROOK J P.
PA (ANDE/) ALSOBROOK J P.
PA (BULD/) BULDGE F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASNAN S J.
PA (CASM/) CASNAN S J.
PA (CASM/) CASNAN L.
PA (CASM/) CASNAN M.
PA (CASM/) MALYANKAR U M.
PA (MALY/) MALYANKAR U M.
PA (MALY/) MALYANKAR U M.
PA (PATY/) PATURAJAN M.
PA (PATY/) PATURAJAN M.
PA (PATY/) PATURAJAN M.
PA (SHIM/) SHENGY S G.
PA (SHIM/) SHENGY S G.
PA (SHIM/) SHENGY S G.
PA (VERN/) VENET C A M.
PA (VERN/) ZERHUSEN B D.
PA (CACAL) SIMILATILY: 75.25%
Best Local Similarity: 75.25%
Percent Similarity:
Best Local Similarity:
Query Match:
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RESULT 393
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15-APR-2004.
(GETH ) GENENTECH INC.
   WO2004031105-A2.
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RESULT 415
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Human DNA35936 used to isolate DNA40628 encoding PRO301 protein.
US2003171568-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX81766 standard; DNA; 390 BP.
Nucleotide sequence of DNA35936 encoding a A33 related antigen.
WO9927098-A2.
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Mismatches:
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Mismatches:
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Consensus assembly expressed sequence tag, EST,
US2002182206-A1.
05-DEC-2002.
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                           ADK40843 standard; cDNA; 721 BP.
DNA encoding human platelet F11 receptor #2
US6699688-B1.
                                                                                                                                                                     AAK92200 standard; cDNA; 605 BP.
Human cDNA 5'-end sequence, SEQ ID NO: 660.
EP1130094-A2.
                                                                                                                                                                                                                                                                                                             5' end of a human cDNA molecule SeqID 660.
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 Indels:
                                                          PN US6699688-BI.
PD 02-MAR-2004.
PA (UYNY ) UNIV NEW YORK STATE RES FOUND.
Percent Similarity: 96.32$ Cons
Best Local Similarity: 97.21$ Mism
Query Match: Indee
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Human PRO301 DNA fragment DNA35936.
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(REAS-2004.

(REAS-) RES ASSOC BIOTECHNOLOGY.

ent Similarity: 92.57%

Local Similarity: 52.57%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX37715 standard; DNA; 390 BP.
Human cDNA clone DNA35936.
                                                                                                                                                                                                   PN EP113cv. PD 05-SEP-2001.
PA (HELL-) HELIX RES INST.
Percent Similarity: 93.14*
Percent Similarity: 92.57*
51.13*
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DD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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100.00%
43.98%
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43.98%
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PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 43.98%
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ADL28627 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ASHK/) ASHKENAZI A.
(FONG/) FONG S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GUDD) GODDARD A. (GURN) GURNEY A I. (NAPL) NAPTER
                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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PA (WOOD/) WOOD W I.
Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                    Query Match:
RESULT 405
Query Match:
RESULT 403
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AAZG1659 standard; cDNA; 403 BP.
cDNA encoding human skin cell transmembrane protein, SEQ ID NO:54.
WO9955865-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human reproductive system related antigen cDNA SEQ ID NO: 712.
WO200155320-A2.
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DNA encoding human prostate cancer antigen, Seq ID No
WO200155316-A2.
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Conservative:
Mismatches:
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Mismatches:
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Human cDNA isolated from skin cells SEQ ID NO:
WO200190357-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Indels:
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Indels:
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Parcent Similarity: 100.00$

Best Local Similarity: 100.00$

7 37.31$
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Percent Similarity: 100.00%
CBest Local Similarity: 37.03.00%
Query Match: 37.31%
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(GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                       AAC99592 standard; cDNA; 403 BP.
Skin cell cDNA, SEQ ID NO: 54.
WO200069884-A2.
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                                                                          DNA; 415 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ent Similarity: 98.21*
Local Similarity: 97.32*
y Match: 35.62*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 98.21%
Best Local Similarity: 97.32%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA06450 standard; cDNA; 425
Human cDNA SEQ ID NO: 116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA; 425
                                                                                         Human AA101561 DNA fragment WO9914241-A2.
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Local Similarity: 100.00%
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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2D 25-MAR-1999.
PAR (GETH) GENENTECH INC.
Percent Similarity: 97.54%
Best Local Similarity: 97.54%
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97.32%
35.62%
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Best Local Similarity: 97.328
Query Match: 35.628
                                      43.98%
                                                                          AAX56510 standard;
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101		121	1 2 2 1	9 9 9	010	000	21 61 17
Conservative: Mismatches: Indels: 16.	Conservative: Mismatches: Indels: ein SEQ ID NO 6.	Conservative: Mismatches: Indels:	gene SeqID71. Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	cDNA EST #264. Conservative: Mismatches: Indels:
PD 02-AUG-2001.  PA (HUMA-) HUMAN GENOME SCI INC.  Percent Similarity: 98.21%  Best Local Similarity: 97.32%  Query Match: 35.62%  RESULT 419  ID ABV83787 standard; cDNA; 425 BP.  DE Human polynucleotide SEQ ID NO 11%  PD 11-UUL-2002.  PA (ROSE/) ROSEN C A.  PA (RUBE/) RUBEN S M.  CRAPA, NARAR S M.	rcent Similarity: 98.21% st Local Similarity: 97.32% st Local Similarity: 97.32% SUL 420 ADB31543 standard; cDNA; 425 BP. Human CDNA encoding a novel prot	1, 7, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	TESOUL #41.  ID ADJ09125 standard; DNA; 425 BP.  DE Human prostate cancer associated PN US2003054373-A1.  PD 20-MAR-2003.  Percent Similarity: 98.21%  Best Local Similarity: 97.32%  Query Match: 35.62%	DE Human T87045 DNA, 435 BP. DE Human T87045 DNA fragment. PN W0991421-A2. PD 25-WAR-1999. PA (GETH) GENENTECH INC. Percent Similarity: 82.43% Best Local Similarity: 80.41% Query Match: 81 Bo.41% RESULT 423 ID AAXS6529 standard; DNA; 322 BP. DE Human 979636 DNA fragment. PN W09914241-A2.	PD 25-MAR-1999. PA (GETH ) GENENTECH INC. Percent Similarity: 99.07% Best Local Similarity: 99.07% Query Match: 34.91% RESULT 424	AAASSOVA BEGINGALI, DAN; 357 Human W76302 DNA fragment. W09914241-A2. 25-WAR-1999. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. 34.12\$ SULT 425 ABA74213 standard; CDNA; 10	mbryonic germ (EG) cell 550-A2. 001. INFGEN INC. arity: 65.18* milarity: 55.80* milarity: 55.80* standard; DNA; 293 BP. one T87045 DNA.

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Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels: Conservative: Mismatches:	Indels: Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	Conservative Mismatches: Indels: adult brain	Conservative: Mismatches: Indels:
W09914241-A2. 25-MAR-1999. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. st. Local Similarity: 97.94% st. Local Similarity: 97.94% SULT 427 ACH30092 standard; cDNA; 416 BP. Human testis cDNA #478. US2003073623-A1. 17-ARR-2003. 17-ARR-2003. (LABA/) LABAT I. (STAC/) STACHE-CRAIN B. (CONE), TANDER T.	PA (UONE) JONES L W PERCENT SIMILARITY: 91.38 BEST LOCAL SIMILARITY: 91.43 QUERY MATCH: 30.31 RESULT 45.28 STANDARY SOUTH AAX56528 STANDARY DE HUMAN RO2633 DNA fragment. PN WO9914241-A2. PD 25-MAR-1999. PA (GETH ) GENENTECH INC. PACETH SIMILARITY: 79 R72 RAST LOCAL SIMILARITY: 79 R72	/ Match: 29.53\$ 24.429 AAX56531 standard; DNA; 269 BP. Human 2328920 DNA fragment. W09914241-A2. CETH ) GENENTECH INC. GETH ) GENENTECH INC. ant Similarity: 100.00\$ Local Similarity: 29.27\$ 7. Match: 29.27\$	2 standard; DNA; 261 BP. 731885 DNA fragment. 1999. GENENTECH INC. 1arity: 100.00% imilarity: 29.02% 2 standard; DNA; 281 BP. 925803 DNA fragment. 41.A2.	INC. 100.00\$ 100.00\$ 28.69\$ DNA, 312 BP. ragment.	CETH ) GENENTECH INC. (GETH ) GENENTECH INC. (GETH 5 imilarity: 97.70% st Local Similarity: 97.70% sry Match: 28.24% SULT 433 AAV82780 standard; cDNA; 1076 BP.	-AAZ. PENETICS INST INC. RILLY: 51.13% Illarity: 35.28%

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AAD44660 standard; cDNA; 1022 BP.
Human secreted protein-encoding gene 25 cDNA clone HTEEB42, SEQ ID NO:35.
US2002077287-A1.
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US2002076756-A1.
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ABZ71351 standard; cDNA; 1022 BP
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PN W09840483-A2.
PD 17-SEP-1998.
A (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 50.16%
Best Local Similarity: 34.19%
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PA (HUMA-) HUMAN GENOME SCI INC.

PECCENT Similarity: 50.16%

Best Local Similarity: '34.19%

Query Match:
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(WELY/) WEL Y.
(MOOR/) MOORE P A.
(YOUN/) YOUNG P E.
(GREE/) GREENE J M.
(FERR/) FERRIE A M.
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FERRIE A M.
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WEI Y.
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ROSEN C A.
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KYAW H.
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(RUBE/) RUBE
(ROSE/) ROSE
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(RUBE/) RUB
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RESULT 442
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RESULT 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ACC72652 standard; cDNA; 1397 BP.
Human vascular endothelial junction-associated molecule cDNA,
WO2003025138-A2.
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               ABQ92017 standard; cDNA; 1076 BP.
Human polynucleotide SEQ ID NO 14
US2002065394-Al.
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Percent Similarity: 51.13 
Best Local Similarity: 35.28 
Query Match: 28.17
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RESULT 441
ID AAV34310 standard; DNA; 1022 BP
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Human clone 2345419 DNA.
WO9914241-A2.
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Human 2345419 DNA fragment.
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Percent Similarity: 51.13*
Best Local Similarity: 35.28*
Query Match: 28.17*
            ID ABG92017 standard; cDNA; 107
DE Human polymucleotide SEQ ID
PU 30-2002065394-A1.
PD 30-MAY-2002.
PA (MCCO/) MCCOY M.
PA (LAVA/) LAVALIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (EVAN/) EVANS C.
PA (REA/) TREACY M.
PA (TREA/) TREACY M.
PA (SPAU/) SPAUDING V.
PA (SPAU/) SPAUDING V.
PECCENT Similarity: 51.13$
Best Local Similarity: 35.28$
QUery MATCh:
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PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 28.11%
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(ACAI Similarity: 100.00%

Match: 28.11%
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Human 1452523 DNA fragment
WO9914241-A2.
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PD 15-APR-2004.
PA (GETH ) GENENTECH IN Percent Similarity: 5 Best Local Similarity: 5 Query Match: 2
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25-MAR-1999.
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RESULT 434
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Human full-length cDNA, SEQ ID NO: 2844.
EP1130094-A2.
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Full length human cDNA clone SeqID 2844.
EP1396543-A2.
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Human NOV2e encoding cDNA SEQ ID NO:27.
WO2004055158-A2.
                                                                                                                                                                                                                                                                                                     ADP69026 standard; cDNA; 939 BP.
Human NOV2b encoding cDNA SEQ ID NO:21.
WO2004055158-A2.
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Human NOV2f encoding cDNA SEQ ID NO:29.
WO2004055158-A2.
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ID ADP68024 standard; cDNA; 952 BP.
DE Human NOV2a encoding cDNA SEQ ID NO:19.
PN WO2004055158-A2.
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DE Full length human cDNA clone Seqi
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 48.38$
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                                                                                                 BP.
                                                                    RESULT 452
ID ADH60143 standard; DNA; 933 B
DE Human JAM 3 DNA.
DE Human JAM 3 DNA.
PN US2003222034-Al.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Percent Similarity: 48.38%
Best Local Similarity: 32.79%
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Human CRAM-1 coding sequence.
WO200053749-A2.
                                                                                                   DNA; 933
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PA (CURA-) CURAGEN CORP.
Percent Similarity: 48.38%
Best Local Similarity: 22.79%
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27.46%
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PA (CURA-) CURAGEN CORP.

Percent Similarity: 48.38%

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PA (CURA-) CURAGEN CORP.

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Percent Similarity: 48.38*
Best Local Similarity: 32.746*
Query Match: 27.46*
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PA (HELL-) HELLY RES INST.
Percent Similarity: 48.3
Best Local Similarity: 32.7
Query Match: 27.4
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(CURA-) CURAGEN CORP.
    Percent Similarity:
Best Local Similarity:
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RESULT 453
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Human junctional adhesion molecule 3 (JAM3) encoding cDNA.
WCJ003006673-A2.
23.-JM-2003.
(TEXA-) TEXAS BIOTECHNOLOGY CORP.
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Human secreted protein-related DNA - SEQ ID 349.
WO2003038063-A2.
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Human cDNA from secreted protein gene 25.
US2003225009-A1.
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Human secreted protein cDNA #SEQ ID 232.
WO2003004622-A2.
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DE Human secreted protein cDNA #SEQ
PN W02003004622-A2.
PD 16-JAN-2003.
PA (HTWA-) HTWAN GENOME SCI INC.
Percent Similarity: 34.19%
Best Local Similarity: 28.04%
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PA (RUBE) RUBEN S M.
PA (ROSE) ROSEN C A.
PA (LIYY) LI Y.
PA (ZENG) ZENG Z.
PA (KYAW) KYAW H.
PA (FISC) FISCHER C L.
PA (LIHH) LI H.
PA (SOPP) SOPPET D R.
PA (GENT) GENTZ R L.
PA (MOOR) MOORE P A.
PA (CREY) WEI Y.
PA (CREE) GREENE A M.
PA (RERR) FERRIE A M.
PA (RERR) FERRIE A M.
PESCLEL SIMILATICY: 28.04%
RESULT 447.
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DE Human junctional adhesion mm w02003008541-A2.
PD W-02003008541-A2.
PA (ELIL ) LILLY & CO ELI.
Percent Similarity: 54.84  
Best Local Similarity: 38.31  
Query Match: 27.72  
RSULT 45.
ID ABZ58994 standard; CDNA; 93:0  
PM W0203006673-A2.
PD W0203006673-A2.
PD A3-JAN-2003.
PA (TEXA-) TEXAS BIOTECHNOLOGY
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ADG89762 8
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RESULT 448
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us-10-785-220b-1.p2n.rng.spdi

ery Match: 27.46% SULT 468	1554 BP. ce SEQ ID NO:261. Conservative:	32.79% 27.46% CDNA. 3654 RD	DE CDNA encoding human PRO1868 polypeptide. PN US2002095507-A1. PP 25-AUL-2002. PA (GETH ) GENENTECH INC.	rcent Similarity: 48.38% st Local Similarity: 32.79% arch: 27.46% SULT 470	ID ABL95691 standard; cDNA; 3554 BP.  DE Human angiogenesis related cDNA PRO1868 SEQ ID NO: 261.  PN W0200208284-A2.  PD 31-JAN-2002.  PA (GETH ) GENENTECH INC.	(BAKE/) (FERR/) (GERB/) (GERR/)	(GODO/) (GURN/) (HILL/) (MARS/)	(PANJ/) PAN J. (PAON/) PAONI N F. (STEP/) STEPHAN J F. (WATA/) WATANABE C	(WIDDA) WILLIAMS F (WOOD) WOOD W I. rcent Similarity: st Local Similarity: ery Match:	RESULT 471  ID ACA60361 standard; cDNA; 3554 BP.  DE Human cDNA for secreted/transmembrane protein PRO1868.  PN 02-130103530-31.	i i i i i	ID ACAD3871 standard; cDNA; 3554 BP. DE CDNA encoding human PRO polypeptide #269. PN US2003036180-A1. PD 20-FEB-2003.	1 t i	RESULY 47.1810 standard; CDNA; 3554 BP.  ID ARX71810 standard; CDNA; 3554 BP.  DE Human CDNA encoding secreted/transmembrane protein PRO1868.  PN US2002132240-A1.	37,5	KESULI 474 ID ACH07141 standard; cDNA; 3554 BP. DE Human secreted/transmembrane polypeptide PRO1868 cDNA.
137 22		.ve: 48 i: 137 22		ve: 48 :: 137 22	Ų	ve: 48 : 137 22	SEQ ID NO:192.	ve: 48 : 137 22		ve: 48 : 137 22 ·	ypeptide.	ve: 48 : 137 22		ve: 48 : 137 : 22	7.	ve: 48 : 137
Mismatches Indels:	S BP.	conservative: Mismatches: Indels:	3515 BP. Lone SeqID 4050.	LOGY. Conservative Mismatches: Indels:	54 BP. an A33 antigen homol	Conservative Mismatches: Indels:		Conservative Mismatches: Indels:	54 BP.	Conservative Mismatches: Indels:	AAS21512 standard; cDNA; 3554 BP. Human cDNA sequence encoding for PRO1868 polypep WO200140466-A2. 07-JUN-2001. (GFH) GRRENTECH INC.	Conservative Mismatches: Indels:	DNA, 3554 BP. secreted protein PRO1868	Conservative: Mismatches: Indels:	54 BP. ecreted protein #7	Conservative: Mismatches:
y: 32.79% 27.46%	cDNA;	y: 32.79% 27.46%	cDNA;	OC BIOTECHNOLOGY 48.38% y: 32.79% 27.46%	rd; cDNA; 3554 ing PRO1868, a	CH INC. 48.38% Y: 32.79% 27.46%	rd; cDNA; 35 rotein UNQ85	CH INC. 48.38% Y: 32.79% 27.46%	rd; cDNA; 3554 DNA.	CH INC. 48.38% Y: 32.79% 27.46%	rd; cDNA; 3554 ence encoding a	y: 32.79% 27.46%	rd; cDNA; 3554 ding secreted;	48.38% Y: 32.79% 27.46%	rd; cDNA; 3554 BP ovel human secret . TNC	48.38\$ 48.38\$ Y: 32.79\$
Best Local Similarity Query Match:		Fercent Similarity: Best Local Similarity: Query Match: RESULT 461	ID ADL32017 standard DE Full length human PN EP1396543-A2. PD 10-MAR-2004.	PA (REAS+) RES ASSOC Percent Similarity: Best Local Similarity: Query Match:	KESULI 462 ID AAA51265 standard, DE Human DNA encoding PN WO200036102-A2. PD 22-JUN-2000	PA (GETH ) GENENTECH INC Percent Similarity: 48 Best Local Similarity: 32 Query Match: 27		PA (GETH ) GENENTECH INC. Percent Similarity: 48. Best Local Similarity: 32. Query Match: 27.	AAF72433 Human Pi WO200104 18-JAN-2	PA (GETH ) GENENTECH INC Percent Similarity: 48 Best Local Similarity: 32 Query Match: 27 RESHLT 465	ID AAS11512 standard; cDi DE Human cDNA sequence ei PN WO200140466-A2. PD 07-JUN-2001.	rcent Simil st Local Si ery Match: SULT 466	ID. ABS68392 standard; CDI DE Human CDNA encoding B: PN US202098566-A1. DD 25-UUL-2002.	rcent Simil st Local Si ery Match:	1D ABS67460 standard; cDNA; 3554 BP. DE cDNA encoding novel human secreted protein PN US2002098505-A1. PD 25-UUL-2002. DA CEPTH ) CENTENDED INC	rcent Simil st Local Si

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17-APR-2003
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RESULT 490
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RESULT 486
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RESULT 487
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RESULT 483
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US200303155-A1.
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US2003036179-A1.
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US2002160374-Al.
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Human secreted/transmembrane protein cDNA, #7.
US2002160392-A1.
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DE CDNA encoding human secreted protein PRO1868.

PN US203023054-A1.

PD 30-JAN-200-100.

PA (GETH) GENENTECH INC.

Percent Similarity: 48.38* Conservativ Best Local Similarity: 32.79* Mismatches: RESULT 480
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US2002164646-Al.
07-NOV-2002.
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ent Similarity: 48.
Local Similarity: 32.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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PN US2002.

PN US2002.

PA (GETH) GENEN.

Percent Similarity:

"Set Local Similarity:

"Match:

"Agen."

"Agen."
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PD 23-JAN-2003.
PA (GETH ) GENENTECH IN Percent Similarity:
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH IN
Percent Similarity: 4
Best Local Similarity: 3
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DNA encoding novel
US2003017563-A1.
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Percent Similarity:
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RESULT 475
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ABX93961 standard; cDNA; 3554 BP.
Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003017463-A1.
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US2003027143-A1.
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RESULT 488
ID ADB29626 standard; cDNA; 3554 BP.
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Human PRO polynucleotide #269.
US200300304517-A1.
20-MAR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
rcent Similarity: 48.38%
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PA (GETH) GENENTECH INC.
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RESULT 485
ID ACD20004 standard;
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US2003049816-A1.
13-MAR-2003.
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8.3

Similarity: 48.38\$ Conservative: 48 aal Similarity: 32.79\$ Mismatches: 137 tch: 27.46\$ Indels: 22	; cDNA; 3554 BP. an PRO polypeptide #269. INC. 48.38\$ Conservative:	32.79%	ADAB6013 standard; cDNA; 3554 BP. Novel human secreted and transmembrane protein PRO1868 cDNA. US2003082693-A1. 01-MAY-2003.	ENENTECH INC.  Irity: 48.38‡ Conservative: 48  iniarity: 32.79\$ Mismatches: 137  27.46\$ Indels: 22	71 501 ADA97225 standard; cDNA; 3554 BP. Human PRO polymucleotide #269. US2003082705-Al.	INC. 48.38% 32.79% 27.46%	andard olynuc 3-Al.	H INC. .48.384 : 32.794 27.464	d; CDNA; 3554 BP. eted and transmembrane protein PR H INC.	48.38% : 32.79% 27.46%	a; cuna; 3554 Br. cleotide #269. H INC.	48.38 32.79 27.46 d: CDNA;	cleotide #61. H INC. Conservative:	Local Similarity: 32.79\$ Mismatches: 137  Match: 27.46\$ Indels: 22  ADMI6458 standard; CDNA; 3554 BP.  Human secreted/transmembrane protein CDNA, #65. 13-MAR.2003. (GETH ) GENENTECH INC. (GETH ) GENENTECH Y: 48.38\$
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27.46%

SUL	ID ADA42603 DE Human sec PN US2003054 PD 20-MAR-20	Fig. 12	DE Human PRO PN US2003077 PD 24-APR-20 PA (GETH ) G	Percent Simila Best Local Sim Query Match: RESULT 517	ID ADA82420 DE Human PRO PN US2003082 PD 01-MAY-20	PA (GETH) G Percent Simila Best Local Sim Query Match: RESULT 518	1D ADA/5383 DE Human PRO PN US2003073 PD 17-APR-20 PA (GETH ) G	9 # 7 B	ADA85461 Novel hu US200308 01-MAY-2	at Ce	ID ADA84909 DE Novel hum PN US20030202 PD 01-MAY-202 PA (GETH ) G Percent Simila	Best Local Sim Query Match: RESULT 521 TD ACD23490		cent Simil st Local Si sry Match:	DE CDNA enco PN US2003073 PD 17-APR-20 PA (GETH ) G Percent Simila Best Local Sim Query Match:
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Best Local Similarity: Query Match:	RESULT 507 ID ADA91962 standard; CDNA; DE Novel human secreted and PN US2003082694-A1.	GENENTECH arity: milarity:		PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	RESULT 509 ID ADB18986 standard; CDNA; DE Novel human secreted and PN US2003073211-A1.	PD 17-APR-2003. PA (GETH) GENENTECH PErcent Similarity: Best Local Similarity: Query Match:	ASSUL 310 ID AD94201 standard; CDNA; 3 DE Human PRO polynucleotide # PN US2003077722-A1. PD 24-APR-2003.	PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	RESOLT 311 ID ADB20097 standard; CDNA; DE Novel human secreted and PN US2003082691-A1.	PD 01-MAY-2003. PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Overy Match:	MESULT 312  ADBLA409 standard; CDNA; DE Human PRO polynucleotide PN 022003082710-A1. PD 01-MAY-2003. PA (GETH) GENENTECH INC.	Percent Similarity: Best Local Similarity: Query Match: RESULT 513	ID ACD98692 standard; cDNA; DE Novel human secreted and PN USZ00304945-A1.	PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	standard O polynuc 8798-A1. 003. GENENTECH arity: milarity:

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standard; cDNA; 3554 BP. man secreted and transmembrane protein PRO1868 cDNA. 2695-A1.
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RESULT 523  ID ADAGOGS standard; CDNA; DE Human PRO polynuclectide PN US200308276.1Al. PD 01-WAY-2003. PA (GETH ) GENENTECH INC. PA SIMILARIY; 48.38% Best Local Similarity; 32.79%	Query Match: RESULT 524 ID ADA75935 standard;	DE Human PRO polymucleotide # PN US2003082703-A1. DD 01-MAY-2003. DA (GRTH ) CRNINNECH INC	Percent Similarity: Best Local Similarity: Query Match:	ID ADA47160 standard; cDNA; DE Human PRO polynucleotide PN US2003073210-A1.	(GETH ) GENENTECH cent Similarity:	Query March: RESULT 526 ID ADB25456 standard;	DE Human PRO polynucleotide PN US2003077715-A1.	CS. ENENTECH rity: ilarity:	Query Match: RESULT 527	ID ADA93632 standard; cDNA; DE Human PRO polynucleotide PN US2003077721-A1.	24-AFK-2003. (GETH ) GENENTECH cent Similarity: st Local Similarity:	Query Match: RESULT 528		PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity:	Query Match: RESULT 529	<pre>ID ADB11269 standard; cDNA; 3554 BP. DE CDNA encoding human PRO polypeptide #269 PN US2003096386-A1.</pre>	PD 22-MAY-2003. PA (GETH ) GENENTECH	Percent Similarity: Best Local Similarity: Query Match:	KESULI 530 ID ACD26813 standard; DNA; 3554 DE CDNA encoding human PRO1868 p DN US200305447-Al.	PD 20-MAR-2003.  PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:

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CDNA; 3554 BP.  NC. 48.38\$ 27.46\$ 27.46\$ CDNA; 3554 BP.  CDNA; 3554 BP.  CDNA; 3554 BP.	CDNA; 3554 BP. Otide #269. NC. 48.38 48.38 27.79 27.46 CDNA; 3554 BP.	NC. 48.38% 32.79% 27.46% CDNA, 3554 BP. Otide #269.			NC. 48.38% 27.46% 27.46% CDNA, 3554 BP. CLIde #269. NC. NG. 38.38%	27.46% CDNA; 3554 BP.
ID ADA61197 standard; DE Homo sapiens. PN US2003049817-A1. PD 13-MAR-2003. Percent Similarity: Best Local Similarity: Guery Match: RESULT 532 DD ADB24344 standard; DE Human PRO polymucl PN US2003077714-A1. PD 24-APR-2003. PA (GETH) GENENTECH PECCENT Similarity: PP (GETH) GENENTECH PECCENT Similarity: PP (GETH) GENENTECH PECCENT Similarity: Percent Similarity: Query Match:	RESULT 533 ID ADA96673 standard; DE Human PRO polymucle PN US200308269-A1. PD 01-MAY-2003 PA (GETH ) GENENTECH II Percent Similarity: Percent Similarity: RESULT 534 ID ADA81245 standard; DE Human PRO polymucle	PN US2003082702-A1. PD 01-WAY-2003. PA (GETH ) GENENTECH I Percent Similarity: Query Match: RESULT 535 ID ADA96121 standard; DE Human PRO polynucle NIS2003082759-A1.	PD 01-MAX-2003.  PA (GETH) GENENTECH INC Percent Similarity: 48 Heet Local Similarity: 37 Query Match: 236 HESULT 536  ID ADB26430 standard; CD DE CDNA encoding human PN US2003082760-Al.	PD 01-MAY-2003. PA (GETH ) GENENTECH IN PERCENT Similarity: Best Local Similarity: Query Match: RESULF 537 ID ADB21915 standard; DE NOVEL Human secrete	PD 01-MAY-2003.  PA (GETH ) GENERTECH   Best Local Similarity: Query Match: RESULT 538  ID AA77694 standard; DE Human PRO polynucle N US2003068797-A1. PD 10-ARR-2003. PA (GETH ) GENERTECH   PR CENT   GENERTECH   PR CENT	W Match LT 539 ADB1843
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ADA87117 standard; cDNA; 3554 BP.
Novel human secreted and transmembrane protein PRO1868 cDNA.
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ADA88220 standard; cDNA; 3554 BP.
Novel human secreted and transmembrane protein PRO1868 cDNA.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
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PA (GETH ) GENENTECH INC.
Percent Similarity: 48.38
Best Local Similarity: 32.79
Query Match: 27.46
RESULT 547
DD ADA43029 standard; CDNA;
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Percent Similarity: 48.
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Query Match: 27.
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PA (GETH ) GENENTECH INC.
Percent Similarity: 48.
Best Local Similarity: 32.
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DE Novel human secreted
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH IN
Percent Similarity: 4
Best Local Similarity: 4
Ouery Match: 2
 DE CDNA encoding human
PN US200307710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH IN
Percent Similarity:
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PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH IN
Percent Similarity:
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ADA88772 standard; cDNA; 3554 BP.
Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003073213-A1.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003027256-A1.
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US2003082706-A1.
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RESULT 549
TD ADB29190 standard; cDNA; 3554 BP.
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sotide #269.
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US2003059909-A1.
                                                                                                                                                PA (GETH ) GENENTECH INC.
Percent Similarity: 48.38*
Best Local Similarity: 32.79*
Oner Match: 27.46*
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PA (GETH ) GENENTECH INC.
Percent Similarity: 48.38*
Best Local Similarity: 32.79*

Query Match: 27.46*
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Best Local Similarity: 32.79%
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US2003082686-A1.
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Percent Similarity: 48...
Best Local Similarity: 32.
PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.

Percent Similarity: 48.

Best Local Similarity: 32.
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PA (GETH ) GENENTECH INC.
Percent Similarity: 48.
Best Local Similarity: 32.
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Percent Similarity: 48.
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                                                                                            ADB28638 standard;
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PD 30-JAN-2003.
Percent Similarity:
Best Local Similarity:
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RESULT 555
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RESULT 553
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% Mismatches: % Indels: 3554 BP. transmembrane protein	rvative: cches: 3:	Onservative: Mismatches: Indels:	Conservative: Mismatches: Indels: BP.	tive: es: tein	Conservative: Mismatches: Indels: BP. protein CDNA, #65.	servative: smatches: lels:	Conservative: Mismatches: Indels: BP. Conservative: Mismatches:
Local Similarity: 32.79% ry Match: 27.46% Jur 564 ADB66749 standard; CDNA; 3554 Novel human secreted and tran	2689-A1. 1003. 1013. 2GENEWIECH INC. 2A:174: 48.388 Milarity: 32.798	standard; cDNA; 3554   Copolynucleotide #269.   26698-A1.   CGENENTECH INC.   GENENTECH INC.   AB.38     milarity: 32.79     27.46     standard; cDNA; 3554   COpolynucleotide #269.   12762-A1.	(GETH ) GENENTECH INC.  LOCAL Similarity: 48.38\$ CONSERVA LOCAL Similarity: 37.79\$ Mismatch: 27.46\$ Indels: AD577947 standard; cDNA; 3554 BP. Human secreted/transmembrane protein cDNA,	S. TENTECH INC.  tty: 48.38%  tarity: 32.79%  27.46%  andard; CDNA; 3554	US2003082764-Al. 01-MXY-2003. int Similarity: 48.38\$ Cor Local Similarity: 32.79\$ Mis ' March: 27.46\$ Inc 'T 569 AbB75083 standard; cDNA; 3554 BP. Human secreted/transmembrane protein	H INC. 48.38% : 32.79% 27.46% d; CDNA;	H INC. 32.79% 27.46% 27.46% 21.0DNA; 21.0DNA; 21.0DNA; 21.0DNA; 33.79%
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SUI SUI	DE Human PRO polynucleotide ## PN US2003064923-A1. PD 03-APR-2003. PA (GETH-) GENENTECH INC. Percent Similarity: 48.38* Best Local Similarity: 32.79* Query Match:	RESULT 557 DE ADAG7158 standard; CDNA; 3554 DE Human PRO polynucleotide #269. PN US2003068793-A1. PD 10-APR-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38* Best Local Similarity: 32.79* QUERY Match: 27.46* RESULT 558 ID ADB23019 standard; CDNA; 3554 DE Human PRO polynucleotide #269. PN US2003077711-A1.	PD 24-ARR-2003.  PERCENT J GENENTECH INC. Percent Similarity: 48.38% Best Local Similarity: 32.79% Query Match: 27.46% RESULT 559 ID ADB23792 standard; CDNA; 31 DE Human PRO polynucleotide Si	8 # 4 #	g 7 7 2	in i	DE Novel human secreted and transmembrane protein PRO1868 PN US2003082766-A1. PD 01-MAY-2003. PA (GETH ) GENENYECH INC. Percent Similarity: 48.38\$ Mismatches: 137 Query Match: 27.46\$ Indels: 22 RESULT 63 ID ADB38277 standard; cDNA; 3554 BP. DE Novel human secreted and transmembrane protein PRO1868 PN US2003087347-A1. PA (GETH ) GENENYECH INC. Percent Similarity: 48.38\$ Conservative: 48

Conservative: 48 Mismatches: 137 Indels: 22

48 137 22

Conservative: 48 Mismatches: 137 Indels: 22

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48 137 22

Conservative: 4 Mismatches: 1 Indels:

NP. :otein cDNA, #65.	Conservative: Mismatches: Indels:	ap. rotein cDNA, #65.	Conservative: Mismatches: Indels:	otein cDNA, #65. Conservative:		otein cDNA, #65.	Conservative: Mismatches: Indels:	BP. protein cDNA, #65.	Conservative: Mismatches: Indels:	otein cDNA, #65.	Conservative: Mismatches: Indels:	t . O	Conservative: Mismatches: Indels:	ap. cotein cDNA, #65.	Conservative: Mismatches: Indels:
1; cDNA; 3554 BP canswembrane pro	48.38% 32.79% 27.46%	1; cDNA; 3554 BP cansmembrane pro	H INC. 48.38% : 32.79% 27.46%	i, cDNA, 3554 E cansmembrane pr inC.	32.79	ansmembrane pro	1 INC. 48.38% 32.79% 27.46%	i, cDNA; 3554 E ransmembrane pr	1 INC. 48.38\$ 32.79\$ 27.46\$	ansmembrane pr	48.38 32.79	cDNA; 3554 nsmembrane INC.	48.38% : 32.79% 27.46%	l, cDNA, 3554 BP ransmembrane pro	
T 580 ADC39930 standard; cDNA; 3554 BP. Human secreted/transmembrane protein cDNA, US2003058828-A1. 27-WAR-2003. (GETH ) GENENTECH INC.	Percent Similarity: Best Local Similarity Query Match: RESULT 581	ADC4044 standard; CDNA; 3554 BP. Aman secreted/transmembrane protein CDNA, US2003059829-Al. CT-YARR-2003. ATTACK-2003.	PA (GETH ) GENENTECT Percent Similarity: Best Local Similarity Query Match: RESULT 582	ID ADC19268 standard; cDNA; 3554 BP. BE Humann secreted/transmembrane protein BN US2003036061-AJ. PD 20-FEB-2003. AA (GETH J) GENENTECH INC. Percent Similarity: 48.38% Con	Best Local Similarity: Query Match: RESULT 583	ADC34399 Standard, CON, 3334 BF. Human secreted/transmembrane protein US2003036094-Al. 20-FEB-2003.	PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match: RESULT 584	ADC29623 standard; cDNA; 3554 BP. Human secreted/transmembrane protein US20031049676-Al. 13-WAR-2003.	PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match: RESULT 585	ADCZ124 Standard; CDNA; 3534 BF. Human secreted/transmembrane protein CDNA, US2003049677-Al. 13-MAR-2003. (GETH ) GENENTECH INC.	Percent Similarity: Best Local Similarity: Query Match: RESULT 586	ADC41039 standard; 3554 Human secreted/transmembrane US2003054400-Al. 20-MAR-2003. (GETH ) GENENTECH INC.	Percent Similarity: Best Local Similarity: Query Match: RESULT 587	ADC19696 standard; cDNA; 3554 BP. Muman secreted/transmembrane protein cDNA, US200305441-A1. COMM. CONTROL OF THE CONTROL OF T	
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27.46% Income CDNA; 3554 BP.	INC. 48.38% 32.79% 27.46%	; cDNA; 3554 BP. leotide SEQ ID NO	INC. 48.38% 32.79% 27.46%	3554 BP. SEQ ID N	.38% .79% .46%	cDNA; 3554 BP.	INC. 48.38% 32.79% 27.46%	; cDNA; 3554 BP. leotide SEQ ID NO	פוה מוה מוה	cDNA; 3554 BP.	INC. 48.38% 32.79% 27.46%	; cDNA; 3554 BP. ted and transmembrane	INC. 48.38% 32.79% 27.46%	; cDNA; 3554 BP. ansmembrane prot	INC. 48.38% 32.79% 27.46%
Query Match: 27.46' RESULT 572 ID ADB77497 standard; CDNA; DE Novel human secreted and PN US2003082696-A1.	ir Ge	andard olynuc 7-Al.	PD 24-APK-2003, AA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	RESULT 574  ID ADB35758 standard; cDNA; DE Human PRO polymuclectide PN US2003077719-A1. PD 24-APR-2003. PA (GETH ) GENENTECH INC.	Percent Similarity: Best Local Similarity: Query Match:	RESOLI 3/3 ID ADB34102 standard, DE Human PRO polynucle PN US2003077716-A1.	24-APR-2003. (GETH ) GENENTECH ccent Similarity: tt Local Similarity: sry Match:	RESULT 576  ID ADB35206 standard; cDNA; BE Human PRO polynucleotide PN US2003077718-A1.	ائع ٿئر ۾	0 standard, RO polynuc] 77720-A1. 2003.	PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	RESULT 578  ID ADB46705 standard; cDNA; DE Novel human secreted and PN US2003082692-A1. PD 01-MAY-2003.	ត្តអង្គ	SULT 579 ADC28730 standard Human secreted/tr	PD 4.7PMAN-2003. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:

Conservative: 48 Mismatches: 137 Indels: 22

Conservative: 48
Mismatches: 137
Indels: 22

48 137 22

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Novel human secreted and transmembrane protein PRO1868 cDNA US2003087367-A1.
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                                    08-MAY-2003
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RESULT 603
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US2003087366-A1.
08-WAY-2003.
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Novel human secreted and transmembrane protein cDNA Seg ID537.
US2003087365-A1.
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US2003092106-A1.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003092105-A1.
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Novel human secreted and transmembrane protein PRO1868
US2003092107-A1.
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Mismatches:
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 ADC34144 standard; cDNA; 3554 BP.
Human secreted/transmembrane protein cDNA, #65.
US2003073077-A1.
                                                                                                                                                ADC13214 standard; cDNA; 3554 BP.
Human secreted/transmembrane protein cDNA, #65.
US2003073079-A1.
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ADC57465 standard; cDNA; 3554 BP.
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PD 15-MAY-2003.
PO (GETH) GENENTECH INC.
Percent Similarity: 48.38%
Best Local Similarity: 32.79%
                                                              GETH) GENENTECH INC.

It Similarity: 48.38%

Local Similarity: 32.79%

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Percent Similarity: 48.38$
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PA (GETH ) GENENTECH INC.
Percent Similarity: 48.
Best Local Similarity: 32.
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ID ADC34144 standard; c
DE Human Secreted/trans
PN US2003077077-A1.
PD 17-ARR-2003.
PA (GETH ) GENENTECH IN
Percent Similarity: 4
Best Local Similarity: 3
Query Match:
RESULT 589
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PD 17-APR-2003.
PA (GETH ) GENENTECH IN Percent Similarity: 4 Best Local Similarity: 2 Query Match: 2
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US2003077657-A1.
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RESULT 596
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ADC54756 standard; cDNA; 3554 BP.
Novel human secreted and transmembrane protein cDNA Seg ID537.
US2003087363-A1.
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Novel human secreted and transmembrane protein cDNA Seg ID537.
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Novel human secreted and transmembrane protein cDNA Seg ID537.
                                                                                  transmembrane protein PRO1868 cDNA.
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Human secreted/transmembrane protein cDNA, #65.
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Percent Similarity: 48.38 Best Local Similarity: 32.79 Query Match: 27.46*
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Percent Similarity; 48.38 Best Local Similarity; 32.79 Process Match: 27.46
                                                                ADC51131 standard; cDNA;
Novel human secreted and
US2003087361-A1.
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PA (GETH) GENENTECH INC.
Percent Similarity: 48.
Best Local Similarity: 32.
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Percent Similarity: 48.
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PA (GETH ) GENENTECH INC.
Percent Similarity: 48.
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(GETH ) GENENTECH INC.
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Percent Similarity: 48
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16-OCT-2003
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RESULT 619
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RESULT 615
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                                                                                                           ADD03362 standard; cDNA; 3554 BP.

Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003092104-A1.
US-MAY-2003.
(GETH ) GENENTECH INC.
CGETH ) GENENTECH INC.
CDCA1 Similarity: 48 Mismatches: 137
Match: 17.46* Indels: 22
                                                                                                                                                                                                                                                   ID ADC90354 standard; cDNA; 3554 BP.

DE Novel human secreted and transmembrane protein PRO1868 cDNA.

PN US2003087348-A1.

PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.

Percent Similarity: 48.38% Conservative: 48

Best Local Similarity: 32.79% Mismatches: 137
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Novel human secreted and transmembrane protein PRO1868 CDNA.
US203087354-A1.
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transmembrane protein PRO1868 cDNA.
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CDNA encoding human PRO polypeptide #269.
US2003194770-A1.
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Human PRO polynucleotide #269.
US2003194773-A1.
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Human PRO polynucleotide #269.
US2003194776-A1.
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PA (GETH) GENENTECH INC.

Percent Similarity: 48.38%

Best Local Similarity: 32.79%

Query Match: 27.46%

RESULT 608
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Novel human secreted and
US2003092103-A1.
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PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 48.3
Best Local Similarity: 32.7
Query Match: 27.4
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PA (GETH) GENENTECH INC.

Percent Similarity: 48.3

Best Local Similarity: 32.7
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
nt Similarity: 48.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENIECH II
Percent Similarity:
Guery Match:
RESULT 605
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Query Match:
RESULT 606
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RESULT 611
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ADC80170 standard; cDNA; 3554 BP.
Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003087358-A1.
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Human secreted/transmembrane PRO polypeptide cDNA #131
US2003105013-A1.
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US2003105011-A1.
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US2003108983-A1.
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RESULT 618

ID ADD09639 standard; CDNA; 3554 BP.

DE Human PRO polynucleotide #269.

PN US2003194775-A1.

PA (GETH) GENEVIECH INC.

PA (GETH) GENEVIECH INC.

Percent Similarity: 48.38$

Best Local Similarity: 32.79$
                                                 Query Match:
RESULT 613
TD ADD10550 standard; cDNA; 3554 BP.
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ADD03803 standard; cDNA; 3554 BP.
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PD 08-MAY-2003.
PD GETH ) GENENTECH INC.
Percent Similarity: 48.38%
Best Local Similarity: 32.79%
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PERCENT SIMILARITY: 48.38%

Best Local Similarity: 32.79%

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Percent Similarity: 48.38%
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PA (GETH ) GENENTECH INC.
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Best Local Similarity: 32.
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PA (GETH) GENENTECH INC. Percent Similarity: 48.38\$ Conservative: 48 B88t Local Similarity: 32.79\$ Mismatches: 137 Query Match: 27.46\$ Indels: 22	codna; 3554 BP. ted and transmembrane protein PR INC. Conservative:	<pre>imilarity: 32.79\$ 27.46\$ 27.46\$ coding human PRO polypeptid 94769-A1. GENENTECH INC. 1arity: 48.38\$ imilarity: 32.79\$</pre>	Indels: 554 BP. Jypeptide #269. Conservative: Mismacches:	3 standard; CDNA; 3554 BP.  10437-A1.  2003. GENENTECH INC.  Canadary 48.38* Conservative: imilarity: 32.79* Mismatches:	2 / 40\$  3 standard, cDNA, 3554 BP. ecreted/transmembrane PRO polypeptide cDNA 2003. GENENTECH INC. 1arity: 48.38\$ Conservative: imilarity: 32.79\$ Mismatches:	939 standard; CDNA; 3554 BP. encoding human PRO polypeptide #269. 3194779-A1. T-2003. ) GENENTECH INC. milarity: 48.38* Conservative: Similarity: 32.79* Mismatches: h:	Machania   Machania

Indels:

	Human Pro Dolynucleotide US2003199026-A1. 23-OCT-2003. (GETH ) GENEWTECH INC. ccent Similarity: 48.38% St Local Similarity: 27.46% STM Match: 27.46% ADM 43287 standard: CDNA.	DE Human PRO polynucleotide # W US2003199033-A1. PD 23-OCT-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38% Query Match: 27.46% RESULT 647	ID ADD96076 standard; cDNA; 3 DE Human PRO polynucleotide # PN US2003199059-A1. PD 23-OCT-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38% Best Local Similarity: 22.79% Query Match:	911 10	1D ADD79080 standard; CDNA; 35 DE CDNA encoding human PRO pol PN USZ003203429-A1. PD 30-OCT-2003. PA (GETH) GENENTECH INC. Percent Similarity: 48.38* Best Local Similarity: 32.79* Query Match: 27.46* RESULT 650 ID ADB33030 standard; CDNA; 35 DE NOVel human secreted and tx	US2003194766-A1. 16-OCT-2003. (GETH ) GENENTECH ccent Similarity: Ext. Local Similarity: STY MAtch: SULT 651 HUMAN PRO POLYNUCL US2003199032-A1.	PD 23-OCT-2003.  PD 23-OCT-2003.  PA (GETH) GENENTECH INC. Percent Similarity: 48.38\$  Best Local Similarity: 32.79\$  Ouery Match: 27.46\$  RESULT 652  ID ADD80738 standard; cDNA; 35  DE cDNA encoding human PRO poll PN US2003207418-11.  PD 66-NOV-2003.  PA (GETH) GENENTECH INC. Percent Similarity: 32.79\$  Query Match: 27.46\$
137 22	48 137 22	48 137 22	PRO1868 cDNA.	22 PRO1868 cDNA. 48 137 22	48 137 22	48 137 22	48 137 22 48 137
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at Local Similarity: 32.79% 27.46% SULT 637	1D ALBLY84 SEAMCHAIN 2524 BF DE HUBELY84 SEAMCHAIN 2520 BF DE HUBELY85 DE HUBELY85 DE HUBELY85 DE HUBELY85 DE HUBELY85 DE HUBER LOCAL SIMILARITY; 48.38 BEST LOCAL SIMILARITY; 27.79 BOUETY MATCH: 27.46 BEST LOCAL SIMILARITY; 27.78 BEST LOCAL SIMILARITY; 27.46 BEST LOCAL SIMILARITY	ID ADD2119 standard; cDNA; 3554 BP DE Human PRO polynucleotide #269. PD 23-OCT-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38% Best Local Similarity: 32.79% GUETY March:	2 standard; uman secrete 94767-Al. 2003. BENENTECH 1 larity: imilarity;	27.46% ard; cDNA; creted and 1. ECH INC. ECH INC. 27.46%	35	Human PRO polynucleotide #2 US2003194768-A1. 16-OCT-2003. (GETH ) GENENTECH INC. (GETH ) Similarity: 48.38 st Local Similarity: 32.794 sry Match: 27.46\$ SULF 643 Human PRO polynucleotide #2	PD 23-0CT-2003. PD 23-0CT-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38\$ COO BEST Local Similarity: 32.79\$ Mit Dest Local Similarity: 27.46\$ InD ADE3505 standard; CDNA; 3554 BP. DE Human secreted/transmembrane protein PN US2003077583-A1. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38\$ COO BEST Local Similarity: 32.79\$

RESULT 645 ID ADE19091 standard; cDNA; 3 DE Human PRO polynucleotide #	cDNA; 3554 BP. otide #269.		
003199026-A1.			
(GETH ) GENENTECH I int Similarity:	1NC. 48.38\$	Conservative:	48
nilarity:		Mismatches:	137
' Match: JT 646	27.46\$	ındels:	77
13287 standard; in PRO polynucle	CDNA; 3554 BP.		
US2003199033-Å1. 23-OCT-2003.			
TH ) GENENTECH I	Š		
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	27.46%	Indels:	22
076 standard;	CDNA; 3554 BP.		
Human PRO polynucle US2003199059-A1.	#		
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int Similarity:	48.38%	Conservative:	84.
Ę	32.79%	Mismarcnes: Indels:	13/
RESULT 648			
122962 Standard; JA encoding human	CDNA; 3554 BF. PRO polypeptide	le #269.	
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larity:	48.38\$		48
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080 standard;	NA; 3554 BP.	1	
US2003203429-A1.	ко ролурерст	ae #269.	
30-OCT-2003.	Ç		
Similarity:	48.38\$	Conservative:	48
al Similarity:	32.79%	Mismatches:	137
atch: 550	27.46%	indels:	22
33030 standard;	3		
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(GETH ) GENENTECH I		9	c v
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andard.	7.5		
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al Similarity:	32.79%	Mismatches:	137
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080738 standard; cDNA;	3554 BP	•	
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Ľ	48.38*	Conservative:	8
al Similarity:	32.79%	Mismatches:	137
, :	27.46%	Indels:	22

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ADG23328 standard; cDNA; 3554 BP.
Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003207384-A1.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
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US2003194777-A1.
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Human PRO polynucleotide #269.
US2003199031-A1.
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RESULT 653
ID ADD89766 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199028-Al.
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ADM55467 standard; CDNA; 3554 BP.
Novel human secreted and transmembrane protein PRO1868 CDNA.
US2003207381-A1.
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Novel human secreted and transmembrane protein PRO1868 CDNA.
US2003207385-Al.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003207386-A1.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003207387-A1.
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   ADG80175 standard; cDNA; 3554 BP.
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ID ADG80175 standard; of Human PRO polynucleo PN US2003207372-A1.
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PA (GETH ) GENENTECH IN Percent Similarity: 4 Best Local Similarity: 3 Query Match: 2 RESULT 662
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ADH81548 standard; CDNA; 3554 BP.
Novel human secreted and transmembrane protein PRO1868 CDNA.
US2003207377-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US2002182618-A1.

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(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO1868 CDNA.
US2003032156-A1.
 Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003207388-A1.
06-NOV-2003.
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cDNA encoding human PRO polypeptide #61.
US2002192659-A1.
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Human PRO polynucleotide #61.
US2002146709-A1.
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DE Novel human secreted PN US2003207388-A1.
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Novel human secreted and transmembrane protein PRO1868 CDNA. US2003087357-A1.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003087353-A1.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003087356-A1.
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US2003087355-A1.
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Novel human secreted and transmembrane protein PRO1868 CDNA.
US2003087385-A1.
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Human secreted/transmembrane protein cDNA, #65.
US20031335025-A1.
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(GETH ) GENENTECH INC.

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Human secreted/transmembrane protein cDNA, #65
US2003148370-AI.
                            Best Local Similarity: 10.30%

Query Match: 27.46%

Mismatches

Query Match: 27.46%

RESULT 694

ID ADE2406 standard; CDNA; 3554 BP.

DE CDNA encoding human PRO polypeptide #269.

PN US2003092110-A1.

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PA (GETH ) GENENTECH INC.

Percent Similarity: 48.38%

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Best Local Similarity: 32.79%

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Query Match: 27.46%

ID ADE24709 standard; CDNA; 3554 BP.

DE CDNA encoding human PRO polypeptide #269.

PN US2003092111-A1.

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DE CDNA encoding human PRO polypeptide #269.

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PN US2003203439-A1.
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DE Human PRO polynucleotide #269.
DN US2003194794-A1.
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PN US2003199054-Al.
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48.38% 32.79% 27.46% CDNA; 3554 BP.	48.38* 32.79\$ 27.46\$ CDNA; 3554 BP.				INC. 48.38% 32.79% 27.46% ; CDNA; 3554 BP.	INC. 48.38% 32.79% 27.46% ; CDNA; 3554 BP	
3 7 7 G	gry r ce	ENTECH ty: arity: andard secret 9-A1.	06-NOV-2003. (GETH ) GENENTECH ccent Similarity: st Local Similarity: sry Match: SULT 753 AD052582 standard NOVEL human secret US2003207414-A1.	US-NOV-ZUUS.  (GETH) GENENTECH Cent Similarity: Local Similarity: PY Match: NULT 754 NOVEL human secret US2003207416-A1.	06-NOV-2003. (GETH ) GENENTECH (GETH Similarity: it Local Similarity: rry Match: NUT 755 NUT 755 HURAD PRO POlynuc' HUMAD PRO POlynuc'	(GETH) GENEWIECH (GETH) GENEWIECH (GETH) GENEWIECH (GETH) GENEWIECH (GETH) Similarity: FY MACCH: NAUSAGES STANDARY MACCHINES	US200320736-AL US200320736-AL (GETH ) GENENTECH (GETH ) GENENTECH STY MATCH: SULT 757 ADH12784 standard NOVEL human secre US200320778-AL. 06-NOV-2003. (GETH ) GENENTECH STMILARITY:

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ndard; cDNA; 3554 BP.
secreted and transmembrane protein PRO1868 cDNA.
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DARD A.
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Mismatches:

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RESULT 777
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Novel human secreted and transmembrane protein PRO1868
US2004009548-A1.
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Novel human secreted and transmembrane protein PRO1868
US2003207382-A1.
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Human secreted/transmembrane protein cDNA, #65.
US2003096340-A1.
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US2003152999-A1.
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082003190610-A1.
09-CCT-2003.
(GETH) GENENTECH INC.
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CDNA encoding human PRO polypeptide #269.
06-NOV-2003.
(GFTH ) GENENTECH INC.
(GFTH ) GENENTECH 1NC.
t Cocal Similarity: 32.79$ Mismatche:
zy Match:
                                                                                                                      Human secreted/transmembrane protein cDNA, US2004005665-A1.
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PD 15-GETH) GENENTECH INC.
Percent Similarity: 48.38%
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PA (GETH) CENENTECH INC.
Percent Similarity: 48.38.
Best Local Similarity: 32.794
Query Match: 27.468
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PD 09-OCT-200.
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PA (GDD/) GODDARD
PA (GNN/) GURNEY A
PA (MXTH/) MATHER J
PA (WACD/) WILLIAMS
PA (WODD/) WOOD W I
PA (WOOD/) WOOD W I
PEXCENT SIMILIANS
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PD 06-NOV-2003.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003207349-A1.
                                                       Novel human secreted and transmembrane protein PRO1868 cDNA.
US2004009547-A1.
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Human secreted/transmembrane protein cDNA, #65.
US2003187238-A1.
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Human secreted/transmembrane protein cDNA, #65.
US2003186358-A1.
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US2004023331-A1.
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RESULT 774
ID AD110340 standard; CDNA; 3554 BP.
DE Human PRO1868 CDNA from DNA77624-2515 clone.
PN US2003228664-A1.
                 Indels:
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ID ADH60794 standard; cDNA; 3554 BP
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ID ADM25385 standard; cDNA; 3554 BP
                                              CDNA; 3554 BP
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(GENT) GENENTECH INC.
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Percent Similarity: 48.38*
Best Local Similarity: 32.79*
Query Match: 27.46*
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(GODO/) GODOWSKI P J.
(GURN) GURNEY A L.
(MATHA) MATHER J P.
(WILL/) WILLIAMS P M.
(WODD/) WOOD W I.
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PA (GETH ) GENENTECH INC.
Percent Similarity: 48.
Best Local Similarity: 32.
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(DESN/) DESNOYERS L.
                                                                                      PD 15-JAN-2004.
PA (GETH ) GENENTECH 1
Percent Similarity:
Best Local Similarity:
                                            ADG09417 standard;
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(GETH ) GENENTECH
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ADI96521 standard; CDNA; 3554 BP.
Novel human secreted and transmembrane protein PRO1868 CDNA.
US2003207354-Al.
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US200413761-A1.
15-UUL-22004.
GETH ) GENENTECH INC.
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cDNA encoding human PRO polypeptide #269.
US2004077064-Al.
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US2003077659-A1.
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ADR11309 standard; cDNA; 3554 BP.
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PA (GETH ) GENENTECH INC.

Percent Similarity: 48.38*

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Query Match: 27.46*
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(GETH ) GENENTECH INC.
ent Similarity: 48.38%
Local Similarity: 32.79%
              PD 03-FEB-2004.

PA (GETH ) GENENTECH INC.

Percent Similarity: 48.

Best Local Similarity: 32.
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BOTSTEIN D.
DESNOYERS L.
EATON D L.
FERRARA N.
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Mismatches:
Human secreted/transmembrane protein cDNA, #65.
US2003096233-A1.
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DE CDNA encoding human PRO polypeptide #269.

PN US200403835-Al.

PD 26-FEB-2004

PA (GETH ) GENENTECH INC.

Percent Similarity: 48.38% Conservati

Best Local Similarity: 27.46% Indels:

RESULT 786
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CDNA encoding human PRO polypeptide #269..
US2004058424.A1.
C5-WAR.-2004.
(GETH ) GENENTECH INC.
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CDNA encoding human PRO polypeptide #269.
US2004048333-A1.
                                                                                                                                                                                                                                       ADM30135 standard; cDNA; 3554 BP.
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US2004038336-A1.
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Human PRO polynucleotide #63.
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US2004043927-A1.
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(GETH ) GENENTECH INC.
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Percent Similarity: 48.
Best Local Similarity: 32.
Query Match: 27.
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(GETH ) GENENTECH INC.
ent Similarity: 48.
Local Similarity: 32.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Local Similarity:
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(GETH ) GENENTECH
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Indels:	BP. protein cDNA, #65.	Conservative: Mismatches: Indels:	tein cDNA, #65.	Concernative	Mismatches:		A #65.																Conservative:	Indels:		CDNA, SEQ ID NO:85		Conservative:	Mismatches: Indels:		clone HAPSA79.		Conservative: Mismatches: Indels:		
27.46%	cDNA; 3554 nsmembrane	INC. 48.38% 32.79% 27.46%	DLI 795 ADT03894 standard; CDNA; 3554 BP. Human secreted/transmembrane prot. US2003152922-A1.	INC.	32.79%	27.40\$	ADS/465/ Brandard; CDNA; 3554 BF. Human secreted/transmembrane CDNA US2004185531-A1.		. A	į.	EI.			Σ Ξ	, n		ر. تان.	•		Α.	>	Ė	48.38%	27.46%	CDNA; 3612		ONT TOO EM	8.38	32.79% 27.46%	4385 BP	gene 13	ME SCI INC.	48.38% 32.79% 27.46%	1; DNA; 4385 BP. gene #38.	
	standa creted/ 8371-A1	2003. GENENTECH larity: imilarity:	4 standard; ecreted/tra 52922-A1.	GENENTECH	sal Similarity:	9	o, standalu; secreted/tra 85531-Al	2004.	ASHKENAZI BOTSTEIN D	DESNOYERS EATON D L.	FERRARA N.	FONG S.	GERBER H.	GERRITSEN M GODDARD A.	GODOWSKI P	GURNEY A I	KLJAVIN I			STEWART T	TUMAS D.	WOOD W I.	Percent Similarity: Bost Local Similarity:		9 stand	Human ovarian anti WO200200677-A1.	03-JAN-2002.	noman Gent larity:	imilarity:	74 standard;	200	(HUMA-) HUMAN GENOME	Percent Similarity: Best Local Similarity: Query Match:	6 standard d protein	WO200107459-A1.
Query Match:	SULT 794 ADI66051 Human se US200314	PD 07-AUG-2003.  PA (GETH ) GENENTEC Percent Similarity: Best Local Similarity: Query Match:	7	14-AUG- (GETH )	Best Local S	SULT 796	DE Human s	23-SEP-					-		(GODO)			(MATH/)		(STEW/)	(TUMA/)	(MOOD/)	rcent Simi	Query Match:	ABQ54979			rce:	st Local S ery Match:	RESULT 798 ID AAC69574	Human s WO20006	(HUMA-)	Percent Simi Best Local S Query Match:	SULT 799 AAF72836 Secreted	WO20010
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RESULT 806
ID AAF72837 standard; DNA; 4386 BP.
DE Secreted protein gene #39.
PN W020107459-A1.
PN W020107459-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 48.38% Mismatches: 13
Ouery Match: 27.46% Indels: 22
RESULT 807
ID ADC73992 standard; DNA; 4386 BP.
DE Human secreted protein-related DNA - SEQ ID 625.
PN W0202038063-A2.
PD 08-MAY-2003.
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Mismatches:
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Human secreted protein encoding sequence #298.
WO200290526-A2.
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DE Human secreted protein gene 13 clone HAPSA79.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (FUMA-) HUMAN 32.79 Wismatches:
Description of the conservative secret. Similarity: 48.38 Mismatches:
Description of the conservative secret. Similarity: 27.74 Mismatches:
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Human secreted protein gene 13 clone HAPSA79.
WO200061623-A1.
                                                                                                                                                                                       ADC73991 standard; DNA; 4385 BP.
Human secreted protein-related DNA - SEQ ID
WO2003038063-A2.
08-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADAS6717 standard; DNA; 4385 BP.
Gene encoding human secreted protein #592.
WO2002102994-A2.
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DE Human secreted protein gene 13 clon w0200061623-A1.
PD 19-CCT-2000.
PA (HOWA-) HUWAN GENOME SCI INC.
Percent Similarity: 48.38*
RESULT 805
DE Secreted protein gene #13.
PD 01-FEB-2001.
PA (HUWA-) HUWAN GENOME SCI INC.
PESCRETE PROTEIN STATE STATE
PD 01-FEB-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 48.38*
Best Local Similarity: 32.79*
Query Match: 27.46*
RESULT 800
ID AD073991 standard; DNA; 4385 BP
DE Human secreted protein-related IP
PN W02003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 48.38*
Query Match: Similarity: 32.79*
Query Match: 2010.
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DE Human secreted protein encoding
PN W0200290526-A2.
PD 14-NVOY-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 48.38%
Query Match:
RESULT 802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID ADAS6717 standard; DNA; 438E
DE Gene encoding human secreted
PN W020210294-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC
Percent Similarity: 48.38%
Dest Local Similarity: 32.79%
Query Match: 27.46%
RESULT 803
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48 137 22 22 48 137 22	48 137 22	48 137 22	48 1137 22	48 137 22	06. 48 137 22	47 138 22
Conservative: Mismatches: Indels: DNA - SEQ ID 401. Conservative: Mismatches: Indels:	BP.  Ig sequence #299.  Conservative: Mismatches: Indels:	. 98	. ŭ	protein #592. Conservative: Mismatches: Indels:	BP. CDNA, SEQ ID NO:106 CONSERVATIVE: 4 Mismatches: 2 Indels: 2	BP. SEQ ID NO:25. Conservative: Mismatches: Indels:
GENOME SCI INC. 48.38  14. 32.79  27.468  ard, DNA, 4386 BP  protein-related 1  2.  GENOME SCI INC. 48.38  12.  48.38  12.  48.38	386 odir NC.	DNA; 4386 in encodin SCI INC. 8.38* 2.79*	NA; 4386 secreted SCI INC. 8.38% 2.79% 7.46%	j DNA; 4386 an secreted DME SCI INC 48.38 32.79 27.46	1; cDNA; 4391 E lecule HISAF60 NOME SCI INC. 48.38 : 32.746\$	EDNA; 3560 Sin gene 15 E SCI INC. 48.05 32.79 27.40 NAA; 387 BF Eragment.
PA (HUMA-) HUMAN GENOME SPECENT Similarity: 48 Best Local Similarity: 32. Query Match: 27. RESULT 808 ID ADC73768 standard; DNA DE Human secreted protein PD 08-MAY-2003. PD 08-MAY-2003. PA (HUMA-) HUMAN GENOME SPECENT Similarity: 48 Best Local Similarity: 48 Query Match: 27	standar reted p 26-A2. 02. JMAN GE rity: llarity	stand creted 526-A2 002. HUMAN arity:	standarding hur 994-A2. 02. UMAN GE rity:	stanc oding 2994-1 102. HUMAN arity arity	standard like mo 30-A2. 02. UMAN GEI rity: ilarity	814 AC74237 stand AC74237 stand anan secreted 2500056754-A1 3-555-2000.  1 Similarity: 5cal Similarity: 5cal Similarity Atch: Atch: A15 A25635 stand A152150 29914241-A2MAR-1999.
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Conservative: Mismatches: Indels:	SEQ ID NO: 209	Conservative: Mismatches: Indels:	ng sequence.	Conservative: Mismatches:	Indels:			Conservative:	Mismatches: Indels:				Conservative:	Mismatches:	indeis:	BP. VEIDM (NOIDM) COND			Conservative:	Mismatches: Indels:		2 splice variant		Conservative:	Indels:				Conservative:	Indels:			Conservative:
100.00% 100.00% 27.20%	coding sequence	50.32% 34.39% 27.17%	cDNA, 1956 BP. noglobulin coding	RM INC. 48.05% 32.79%	27.14%	DNA, 252 BP. fragment.	Ç.	96.438	96.43% 27.07%	DNA; 260 BP.	fragment.		INC. 100.	100.00\$	27.01\$	CDNA; 1389 BP.	3		50.81%	26.98	CDNA;	sion molecule	1.10		26.88	NA; 194	sequence	ENE SA.	50.68%	26.88\$	NA; 194	sequence	ENE SA. 50.68%
Percent Similarity: Best Local Similarity: Ouery Match:	816 AH98352 standard; uman EST-derived 0200154477-A2.	-AUG-2001. ISE-) HYSEQ INC. Similarity: cal Similarity: atch:	AAA27386 standard; cDNA; 19: Human IGFAM-6 immunoglobull: WO200029583-A2.	PD 25-MAY-2000. PA (INCY-) INCYTE PHAP Percent Similarity: Best Local Similarity:	Match:	standard;	ŧ	Similarity:	ocal Similarity: fatch:	AX56517 standard;	Human 3236257 DNA W09914241-A2	5-MAR-1999.	GENENTECH larity:	cal Similarity:	atch: 820	AAL60897 standard;	16180-A2.	05-JUN-2003. (GEST ) GENSET SA.	ilarity:	Local Similarity: / Match:	RESULT 821 ID ADP56686 standard;	ction adh	24-JUN-2004.	larity:	atcl	822 A9718	3749-A	14-SEP-2000. (RMFD-) RMF DICTAGENE		ocai Similailey: Match:		Murine CRAM-1 codir WO200053749-A2.	MFD- Sin
Percent Best Lo Query M	<u>,</u>	PD 02. PA (H) Percent Best Loc Query M	I DE P	PD PA PERCEI	Query RESUL ₁	OIO		Percent	Best I Query	Š	DE		ព	Best I	ťΈ	OI C		PA C	Percer	Duery	RESULT ID P	DB	200	(I)	Ouery M	ID A		PD PA	Percer	Query Match	RESULT ID A	PNE	rcei

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Mismatches: Indels:	ed in lung cancer	Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:	8-1141.	Conservative:	nismacches: Indels:	95 BP. encoding cDNA SEQ ID		Conservative: Mismatches: Indele:		cDNA, UNQ219.		Conservative: Mismatches: Indels:		Conservative: Mismatches:	Indels:		Conservative: Mismatches: Indels:	Conservative: Mismatches:
33.78% 26.88%	cDNA; 3717 BP. ntially expressed	49.16% 33.11% 26.88%	CDNA; 1295 BP.	INC. 50.85% 35.15% 26.42%	DNA; 1295 BP. A clone DNA35638	INC. 50.85%	26.42#	cDNA; 1295 BP. in UNQ219 encod	Ç	1MC. 50.85% 35.15% 26.42%	CDNA; 1295	in encoding	INC.	35.15% 26.42%	cDNA; 1295 BP. sequence SEQ ID	INC. 50.85% 35.15%	26.42%	cDNA; 1295 BP.	INC. 50.85% 35.15% 26.42%	CDNA, 1295 BP. INC. 50.85% 35.15%
Best Local Similarity: Query Match:	KESULT B 24 ID ACHO4172 standard; cDNA; 37 DE Human cDNA differentially e PP US2003065157-A1. PD 03-ARR-2003.	PA (LASE/) LASEK A W. Percent Similarity: Best Local Similarity: Query Match:	KESULT 825 ID AAX37664 standard; DE Human PRO245 CDNA. PN WO9914241-A2. PD 25-MAR-1999.	PA (GETH) GENERIECH Percent Similarity: Best Local Similarity: Query Match:	RESULT 826 ID AAXS2225 standard, D DE Protein PRO245 cDNA PN WO9914328-A2	39. SNENTECH	Dest Docal Similarity: Query Match:	ID AACS886 standard; cDNA; 129 DE Human PRO245 protein UNQ219	PD 14-SEP-2000.		RESULT 828 ID AAZ52202 standard;	DE Human PRO245 prote PN WO200015797-A2.	PD 23-MAR-2000. PA (GETH ) GENENTECH :	Fercent Similarity: Best Local Similarity: Query Match:	RESULT 829  ID AAA77562 standard; DE Human PRO245 cDNA 8  PN WO200032221-A2.		Query Match: RESULT 830	ADC78383 standard Human PRO245 cDNA. WO200015796-A2. 23-MAR-2000.	PA (GETH ) GENENTECH Percent Similarity: Query Match: Degriff 921	ID AAF 2383 standard; DE Human PRO245 cDNA. PN WO200104311-A1. PD 18-JAN-2001. PA (GETH) GENEWECH I Percent Similarity: Best Local Similarity:

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AAC97437 standard; cDNA; 1295 BP.
Human angiogenesis-associated protein PRO245 cDNA, SEQ ID NO:90.
WO200053753-A2.
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BESULT 837

CALO7452 standard; CDNA; 1295 BP.

D ACC07452 standard; CDNA; 1295 BP.

N US2002197671-Al.

N US2002197671-Al.

A (GETH ) GENENTECH INC.

ercent Similarity: 35.15% Mismatches: 128

ESULT 838
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US2002132240-A1.
19-SEP-2002.
(GETH ) GENENTECH INC.
AAS00157 standard; cDNA; 1295 BP.
Human cDNA clone DNA35638-1141 encoding PRO245 (UNQ219).
WO200119991-A1.
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128
16
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Human cDNA for secreted/transmembrane protein PRO245.
US2003003530-A1.
                                                                                                                                      AASZ1411 standard; cDNA; 1295 BP.

E Human cDNA sequence encoding for PRO245 polypeptide.

N WO200140466-A2.

O 77-JUN-2001.

A (GETH ) GENENTECH INC.

PETCENT Similarity: 50.85% CONSERVATIVE: 46

BST LOCAL Similarity: 35.15% Mismatches: 128

LOCAL 834.
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Mismatches:
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cDNA encoding human PRO polypeptide #168.
US2003036180-A1.
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 835
ID AAC91463 standard; cDNA; 1295 BP.
B Human PRO245 cDNA.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH) GRNENTECH INC.
Percent Similarity: 50.85%
Best Local Similarity: 35.15%
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                                     'N mccoccation 22-Mar-2001.
PA (GETH ) GENENTECH INC.
Percent Similarity: 50.85%
Best Local Similarity: 35.15%
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(GETH ) GENENTECH INC.
streent Similarity: 50.85$
est Local Similarity: 25.15$
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ercent Similarity: 50.85%
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ascur Match: 26.42%
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ESULT 833
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RESULT 840 ID ACH06832 standard; CDNA; 1295 BP. DE Human secreted/transmembrane polypeptide PN US2003044839-A1.	cDNA; 1295 ВР. ывмемbrane polyp	PR0245	cdna.		ID ACA54860 standard; cDNA; DE Novel human secreted and PD US2003017463-A1. PD 23-JAN-2003.	cDNA; 1295 BP. ed and transmembrane	protein	PRO245 cDNA.
rce ery	INC. 50.85% 35.15% 26.42%	ative: hes:	46 128 16		(GETH ) GENENTECH rcent Similarity: et Local Similarity: ery Match: SULT 849	INC. 50.85\$ 35.15\$ 26.42\$	Conservative: Mismatches: Indels:	46 128 16
SULT 841 ABX89308 standard; DNA encoding novel US2003017563-A1.	CDNA; 1295 BP. secreted and transmembrane	pr	otein PRO245.		ACD19695 standard Human secreted / US2003027143-A1. 06-FEB-2003.	; cDNA; 1295 BP. transmembrane polypeptide	PR024	5 cDNA.
PD 23-JAN-2003. PA (GETH ) GENENTECH I Percent Similarity: Best Local Similarity: Query Match:	INC. 50.85\$ 35.15\$ 26.42\$	Conservative: Mismatches: Indels:	128 , , , , , , , , , , , , , , , , , , ,		(GETH ) GENENTECH crent Similarity: st Local Similarity: sty Match: SULT 850	<b></b>	Conservative: Mismatches: Indels:	46 128 16
2 standard; ecreted/trar 36179-A1.	cDNA; 1295 BP. nsmembrane prote	CDNA	#168.		ADA45854 standard; Novel human secret US2003022328-A1. 30-JAN-2003.		1295 BP. transmembrane protein PRO245	10245 CDNA.
B-2003.   ) GENENTECH		Conservative: Mismatches: Indels:	46 128 16		SENENTECH arity: nilarity:	NC. 50.85% 35.15% 26.42%	Conservative: Mismatches: Indels:	46 128 16
KESULT 843  1D ABX96063 standard; CDNA; 1295 BP. DE Human secreted/transmembrane protein PN US2003160314-A1. PD 31-OCT-2002	cDNA; 1295 BP. ısmembrane prote	in cDNA, #13.		<del></del>	ID ADA'6285 standard; of Human PRO polynucle PN US2003073212-A1. PD I7-APR-2003.	cDNA; 1295 BP.  leotide #168.   TNC		
(GETH ) GENENTECH coent Similarity: st Local Similarity:	INC. 50.85% 35.15% 26.42%	Conservative: Mismatches: Indels:	46 128 16		Percent Similarity: Best Local Similarity: Query Match: RESULT 852	350.85 35.15\$ 26.42\$	Conservative: Mismatches: Indels:	46 128 16
. 5	cDNA; 1295 BP. 1 secreted prote	in PRO245.			ADB29268 standard Human secreted/tr; US2003092002-A1. 15-MAY-2003.	cDNA; 1295 BP. nsmembrane prote	in cDNA, #13.	
PD 30-JAN-2003.  PA (GETH ) GENENTECH INC.  Secont Similarity: 50 85%  Best Local Similarity: 35.15%  Query Match: 26.42%		Conservative: Mismatches: Indels:	46 128 16		PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match: RESULT 853	NC. 50.85% 35.15% 26.42%	Conservative: Mismatches: Indels:	46 128 16
7 standard ecreted / 36060-A1. 2003. GENENTECH	l; cDNA; 1295 BP. transmembrane polypeptide   INC.	PR024	cDNA.	.,	ਜਹੇਹ ਲ	cDNA; 1295 BP. otide #168. NC.	Conservative:	<u>م</u> 70
larity: imilarity: 8 standard;	0.85% 15.15% 6.42% DNA; 1295 BP.		46 128 16		# ÇÇ	35.15% 26.42% CDNA; 1295 BP.	Mismatches: Indels:	128 16
CDNA encoding human US2002182206-A1. US-DEC-2002. (GETH ) GENENTECH : ccent Similarity: st Local similarity:	A-33 related IC. io.85% 5.15% 6.42%	antigen PRO245. Conservative: Mismatches: Indels:	446 128 16			INC. 50.85% 35.15% 26.42%	Conservative: Mismatches: Indels:	46 128 16
1 standard; DNA encoding 32155-Al.	cDNA; 1295 BP. g a secreted/transmembrane	pro	tein, SEQ ID 335.		3 standard; uman secret 68796-Al. 2003.	cDNA; 1295 BP.	protein	PRO245 CDNA.
GETH ) GENERATECH I COERT SIMILARITY: St Local Similarity: Pry Match: SULT 848	85\$ 15\$ 42\$	Conservative: Mismatches: Indels:	46 128 16		cent Similarity: st Local Similarity: sry Match: SULT 856 ADB27884 standard;	50.85% 35.15% 26.42% CDNA, 1295 BP.	Conservative: Mismatches: Indels:	46 128 16

US2003082693-A1.

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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003082711-A1.
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ADA85811 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
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US2003045693-A1.
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TEB-21003.
(GETH ) GENENTECH INC.
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US2003068794-Al.
cDNA encoding human PRO polypeptide #168.
US2003082704-A1.
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Human PRO polynucleotide #168.
US2003068795-A1.
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Human PRO polynucleotide #168.
US2003073215-Al.
17-APR-2003.
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06-MAR-2003.
(GETH ) GENENTECH INC.
rcent Similarity: 50.85%
  DE CDNA encoding human PRO pol:
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 50.85%
Best Local Similarity: 35.15%
Query Match: 26.42%
RESULT 857
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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B Human secreted/trans
PN US200303971-A1.
PD 27-FEB-2003.
PA (GETH) GENERATECH IN
Percent Similarity: 3
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PD 01-MAY-2003.
PA (GETH) GENENTECH IN Sercent Similarity: 5 Best Local Similarity: 5 Query Match: 2
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PD 08-MAY-2003.
PA (GETH ) GENENTECH IN Percent Similarity: 5 Best Local Similarity: 5 Query Match: 25 March: 25 
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PD 10-APR-2003.
PA (GETH) GENENTECH IN
Percent Similarity:
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PD 06-MAR-2003.
PA (GETH) GENENTECH IN
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PD 10-1
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Percent
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DE Novel human secreted and transmembrane protein PRO245 CDNA. PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 50.85*
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Novel human secreted and transmembrane protein PRO245 cDNA.
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Human secreted/transmembrane protein cDNA, #13
US2003049621-A1.
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US2003044793-A1.
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Human PRO polynucleotide #168.
US2003087351-A1.
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В
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Human PRO polynucleotide #168.
US2003082705-A1.
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Human PRO polynucleotide #168.
US2003087349-A1.
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US2003082763-A1.
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PD 08-MAY-2003.

PA (GETH ) GENENTECH INC. Percent Similarity: 50.85% Best Local Similarity: 26.42%
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PA (GETH ) GENENTECH INC.

Percent Similarity: 50.85*

Best Local Similarity: 35.15*

Query Match: 26.42*
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DE Human sec...
PN US2003049621-Ai..
PD 13-MAR-2003.
PA (GETH) GENENTECH INC..
Percent Similarity: 50.8'
Best Local Similarity: 35...
"Ary Match: "Tandard; c
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PA (GETH ) GENENTECH INC.
Percent Similarity: 50.
Best Local Similarity: 35.
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(GETH ) GENENTECH INC.
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RESULT 869
ID ACD83003 standard;
OB Human PRO polynucleo
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH IN
Percent Similarity: 3
Best Local Similarity: 3
PD 01-MAY-2003.
PA (GETH ) GENENTECH
Percent Similarity:
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Query Match:
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RESULT 866
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RESULT 868
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PD 08-MAY-2003. PA (GETH) GENENTECH INC. Percent Similarity: 50.85% Conservative: 46 Best Local Similarity: 35.15% Mismatches: 128 Query Match: 26.42% Indels: 16	ID ADB18784 standard; cDNA; 1295 BP. DE Novel human secreted and transmembrane protein PRO245 cDNA. PN US2003073211.Al. PD 17-APR-2003.	PA (GETH) GENENTECH INC.  Percent Similarity: 50.8\$ Conservative: 46  Best Local Similarity: 35.1S\$ Mismatches: 128  Query Match: 26.42\$ Indels: 16	SULT 874 ADA33999 standard; cDNA; 1295 BP. ADA33999 standard; cDNA; 1295 BP. Human PRO polynucleotide #168. US20033077722-A1. 24-APR-2003.	PA (GETH ) GENENTECH INC. Percent Similarity: 50.85\$ Conservative: 46 Best Local Similarity: 35.15\$ Mismatches: 128 Query Match: 26.42\$ Indels: 16	andard; cDNA; 1295 BP. secreted and transmembrane protein P 1-A1.	PD ULTMAT-2003. PA (GETH) GENENTECH INC. Percent Similarity: 50.8% Conservative: 46 Best Local Similarity: 35.15% Mismatches: 128 Query Match: 26.42% Indels: 16	ADB13207 standard; cDNA; 1295 BP. Human PRO polynucleotide #168.	PN 022003082710-A1. PD 01-MAY-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 50.85* Conservative: 46 Best Local Similarity: 35.15\$* Mismatches: 128 Chary March 726.42* Indels: 16	SULT 877 ACD98591 standard; CDNA; 1295 BP. Novel human secreted and transmembrane protein PRC US220344945-Al.	PD 06-MAR-2003.  PA (GETH) GENENTECH INC.  Percent Similarity: 50.85\$ Conservative: 46  Best Local Similarity: 35.15\$ Mismatches: 128  OMETY MATCH: 26.42\$ Indels: 16	l standard; cDNA; 1295 BP. RO polynucleotide #168. 68798-Al.	PD 10-APR-2003. PA (GETH) GENENTECH INC. Percent Similarity: 50.85\$ Conservative: 46 Best Local Similarity: 35.15\$ Mismatches: 128 Query Match: 26.42\$ Indels: 16	4 standard ecreted/tra 54401-A1. 2003.	PA (GETH ) CENENTECH INC. Percent Similarity: 35.15\$ Conservative: 46 Best Local Similarity: 35.15\$ Mismatches: 128 Query March: 26.42\$ Indels: 16 ·	TESUL 800 ID ADE24694 standard; CDNA; 1295 BP. DE Human PRO polynucleotide SEQ ID NO 335. PN US2003077713-Al. PD 24-APR-2003.

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st Local Similarity: 35.15% SILL 897 ADAB1043 standard; CDNA; 1295 BP. Human PRO polynucleotide #168. US2003082702-A1. 01-MAY-2003. GETH ) GENENTECH INC. GETH ) GENENTECH Similarity: 50.85% st Local Similarity: 50.85% ery Match: 26.42% SULT 898	RO perandard; cDNA; 1295 BP. RO polynucleotide #168. 82759-A1. GENENTECH INC. 1arity: 50.85\$ imilarity: 35.15\$ 8 standard; cDNA; 1295 BP. coding human PRO polypeptig 2003. 2003. 62760-A1. 2003. 62760-A1. 50.85\$ imilarity: 50.85\$ imilarity: 35.15\$	Match:  26.42*  Amatch:  Amatch:  Amatch:  Bools Standard; CDNA; 1295 BP.  Novel human secreted and transmemt  US2003082765-Al.  O1-MAY-2003.  GETH   GENERYECH INC.  Standarity:  Coal Similarity:  Match:  Amatch:  Amatc	Manan PRO polymucleotide #168.  Manan PRO polymucleotide #168.  JAPR-2003.  BETH ) GENENTECH INC.  Similarity: 50.85\$  Acal Similarity: 56.42\$  BB18212 standard; cDNA; 1295 BP.  NNA encoding human PRO polypeptic  SIMILARITY.  SIMILARITY.  SIMILARITY.  SIMILARITY.  SIMILARITY.  SOURCE SOURCE SOURCE SOURCE SIMILARITY.  SOURCE SOUR

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Query Match:	RESULT 905 ID ADA12952 standard; CDNA; 1295 BP. DE Human secreted/Lransmembrane protein CDNA, PN US2003049622-A1.		Ę	003. GENENTECH arity: milarity:	RESULT 907  ID ADA88018 standard; cDNA; DE Novel human secreted and PN US2003082700-A1.	003. GENENTECH arity: milarity:	ID ADA46406 standard; cDNA; DE Novel human secreted and	3 7 7	KESOLI 303 ID ADA17167 standard; CDNA; 1295 BP. DE Human secreted/transmembrane protein CDNA, DN IRSON1017498-11	PD 23-JAN-2003. PA (GETH ) GENENTECH : Percent Similarity: Best Local Similarity: Query Match:	resold 310 ID ADA42670 standard; cDNA; 1295 BP. DE Human secreted/transmembrane protein cDNA, PN US2003054351-A1.	PD 20-MAR-2003.  Dercent Similarity: Best Local Similarity: Query Match:	ABSORATE Standard; CDNA; 1295 BP. DE CDNA encoding human PRO polypeptide #168 PP. US2003082699-A1.	(GETH ) GENENTECH cent Similarity: st Local Similarity:	KESULF 912 ID ADB28988 standard; CDNA, DE CDNA encoding human PRO PN US2003082766-A1. PD 01-MAY-2003.	(GETH ) GENENTECH coent Similarity: st Local Similarity: srv March.

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MARSS 10 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US200307313-A1.
17-ARR-2003
(GETH ) GENENTECH INC.
Conservative: 46
Fr Local Similarity: 35.15* Mismatches: 128
SULT 915
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ADB23590 standard; cDNA; 1295 BP.
Human PRO polynucleotide SEQ ID NO 335.
SULT 913
ADA76940 standard; cDNA; 1295 BP.
Human PRO polynucleotide #168.
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ADA66956 standard; cDNA; 1295 BP.
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US2003082686-A1.
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1D ADB38075 standard, cDNA; 1295 BP.

DE Novel human secreted and transmembrane protein PRO245 cDNA.

DN US200387347-A1.

PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.

Percent Similarity: 50.85$ Conservative: 46

Best Local Similarity: 35.15$ Mismatches: 128

Query Match: 16
                                                                                                   ADA92312 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003082766-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US20031082689-A1.
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Human PRO polynucleotide #168.
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Percent Similarity: 9
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ADB39460 standard, cDNA, 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
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RESULT 934
ID ADB77295 standard; CDNA; 1295 BP.
DB Novel human secreted and transmembrane protein PN US2003082696-A1.
                                                                                                                                                                                                                     Human secreted/transmembrane protein cDNA, #13 US2003082542-A1.
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Human PRO polynucleotide SEQ ID NO 335.
US2003077719-Al.
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US200307716-A1.
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RESULT 933
ID ADB66590 standard; cDNA; recomment PRO polynucleotide #1
on US2003082697-A1.
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Percent Similarity: 50.85% Best Local Similarity: 35.15% Query Match: 26.42% RESULT 946 ID ADC29244 standard; cDNA; 1: DE Human secreted/transmembrai PN US2003049676-A1. PD 13-MAR-2003.		PD 13-MAR-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 50.85% Best Local Similarity: 35.15% Query Match: 26.42% RESULT 948 ID ADC40680 standard; cDNA; 1: DE Human secreted/transmembran PN US2003054400-A1. PD 20-MAR-2003.	g # # g	2 # # E	Human secreted/trafy US200307307-A1. 17-APR-2003. (GETH ) GENENTECH I ccent Similarity: st Local Similarity: sty Match: ULT 951.		ID ADC50376 standard; CDNA; 12 DE Novel human secreted and ti PN US2003092106-A1. PD 15-WAY-2003. PA (GETH) GENENTECH INC. Percent Similarity: 50.85% Query Match: 50.85% RESULT 953 ID ADC71923 standard; CDNA; 12	
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rce sry Sul	PD 24-APR-2003.  PA (GETH ) GENENTECH INC. Percent Similarity: 50.854 Query Match: 26.424 RESULT 939 ID ADB36108 standard; cDNA; DE Human PRO polynucleotide	SULY ST	PD 01-MAY-2003.  PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match: RESULT 941  ID ADC28371 standard DR Human specreted/try	PN US2003059772-A1. PD 27-MAR-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 50.85% Cor Best Local Similarity: 35.15% Mis Query Match: 26.42% In	571 standard secreted/tr 3059828-A1. R-2003. N GENENTECH milarity: Similarity:	085 standard secreted/tr. 3059829-A1. R-2003. Milarity: Similarity:	KESULI 944  ID ADC18913 standard; CDNA; 1295  DE Human secreted/transmembrane PN US2003036061-A1.  PD 3C-FEB-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 50.85\$  Best Local Similarity: 35.15\$  QUETY MATCH: 26.42\$  TRESULT 9455	AUC34209 Stand Human secreted US200336094-7 20-FEB-2003.

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Percent Similarity: Best Local Similarity: Query Match: RESULT 946	ADC29264 standard; cDNA; 1299 Human secreted/transmembrane US2003049676-A1.	a)	y Match:	ADC28795 standard; cDNA; 1295 Human secreted/transmembrane US2003049677-A1.	13-MAR-2003. (GETH ) GENENTECH	Local Similarity:	Query Match: RESULT 948		m ~	HIS	Local Similarity:	Query Match: RESILL 949	ADC19337 standard; cDNA; 129	Human secreted/tra .US2003054441-A1.	20-MAR-2003.	ent Simil	Local	RESULT 950	ADC33785 Standard, Human secreted/tra	US2003073077-A1.	(GETH ) GENENTECH	ent Similarity:	Matcl	951 X12855		17-APR-2003. 17-APR-2003. (GETH ) GENENTECH	ent Simil	Locai Similarity: y Match:	RESULT 952 ID ADC50376 standard;	Novel human secret US2003092106-A1.	15-MAY-2003. (GETH ) GENENTECH IN	ent Similarity:	ğŸ	LT 953 ADC71923 standard;	Novel numan secreted US2003092107-A1.	(GETH ) GENENTECH	-
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ery Match: SULT 962	DE NOVEL human DE NOVEL human PN US2003087355 PD 08-MAY-2003.	S to the		g tr	ID ADC58486 sta DB Novel human PN US2003087346 PD 08-MAY-2003	rcent Similst Local Similst Local Similst Sury Match:	Human sec US2003082 01-MAY-2(	Sty St		(GETH ) C rcent Simila st Local Sin ery Match: SULT 967	1D ADC90152 SE DE Novel human PN US2003087346 PD 08-MAY-2003	gr te	CDNA encc US2003194 16-OCT-20	PA (GETH ) GEN Percent Similarit Best Local Simila Query Match: RESULT 969	DE Human PRO pc PN US200319477 PD 16-OCT-2003	rcent Simi st Local S: ery Match:
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ADD03868 standard; CDNA; 1295 Human secreted/transmembrane iUS2003104381-A1. 05-UUN-2003. (GETH ) GENENTECH INC. (GETH ) Similarity: 50.85\$ st Local Similarity: 35.15\$ sry Match: 26.42\$ SULT 979	1D ADD03448 tacandard; CDNA; 1295 BF.  DE Human secreted/transmembrane prote PN US2003108983-A1.  PD 12-JUN-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 50.85%  Query Match:  RESULT 980	AD541150 standard; cDNA; 1295 Novel human secreted and trans US2003203438-A1. 30-OCT-2003. (GETH ) GENENTECH INC. cent Similarity: 50.85% sty Local Similarity: 35.15% SUF SULT 981.	ID ADD52289 standard; cDNN; 1295 BP. DE CDNA encoding human PRO polypeptid PN US2001194769-A1. PD 16-OCT-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 50.85* Best Guery Match: 35.15* Query Match: 26.42*	D ADD53029 Brandard; CDNA; 1259 Br.  DE CDNA encoding human PRO polypeptid PN US2003194792-A1.  PD 16-OCT-2003.  PA (GETH) GENEWTECH INC.  Percent Similarity: 50.85% Best Local Similarity: 26.42%  RESULT Match: 26.42%	DE Novel human secreted and transmember VS2003203437-A1.  PD 30-OCT2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 50.85%  Best Local Similarity: 35.15%  Query Match:  RESULT 984  TO ADD5/177 standard: CDNA: 1295 BP.	an PRO polype INC. 50.85% 35.15% 26.42%	ID ADD02536 standard; cDNA; 1295 BP.  DE Human PRO polynucleotide #168.  PN US2003203431-A1.  PD 30-OCT-2003.  PA '(CETH) GENEWYECH INC.  Percent Similarity: 50.85%  Best Local Similarity: 26.42%  RESULT 986  ID ADD01970 standard; CDNA; 1295 BP.
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RESULT 970  ID ADD09989 standard; cD  ID Human PRO polynucleot  PN US200319476-A1.  PD 16-OCT-2003.  PP (GFTH) GENENTECH INC  Percent Similarity: 55  Best Local Similarity: 35  Query Match: 26	4 standard; uman secret 87354-A1. 2003. GENENTECH larity: imilarity:	0 standard; uman secret 92103-Al. 2003. GENENTECH larity: imilarity:	Petandard, RO polynucl 94774-A1. 2003. GENENTECH larity: imilarity:	8 standard; RO polynucl 94771-A1. 2003. GENENTECH larity: imilarity:	862 standard, secreted/trs 3104469-A1. N-2003. milarity: Similarity:	968 standard, human secret 3087358-A1. Y-2003. ) GENENTECH milarity: Similarity:	RESULT 977  RESULT 977  D ADD09437 standard; CD  DB Human PRO polynucleot  PN US2003194775-A1.  PD 16-OCT-2003.  PA (GETH ) GENENTECH INC  Percent Similarity: 50  Best Local Similarity: 35  Query Match: 26  RESULT 978

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trandard; cDNA; 1295 BP. In secreted and transmembrane protein PRO245 cDNA. 37-A1.
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In secreted and transmembrane protein PRO245 cDNA.
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Sand Dorymon. 20132003. ) GENENTECH illarity: Similarity:	AESOLI 98/ ID ADD54152 standard; cDNA; DE Novel human secreted and PN US2003203432-A1.	-2003. ) GENENTECH ilarity: Similarity:	RESULT 988  ID AD92469 standard; CDNA; DE Human PRO polynucleotide PN US2003199030-A1. PD 23-OCT-2003. PA (GETH) GENENTECH INC. Percent Similarity: 35.15% Query Match: 26.42%	KESULT 989 LD ADD91365 Standard; CDNA; DE Human PRO polynucleotide PN US2003199055-A1. PD 23-OCT-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 50.85; Guery Match:	KESULI 990 ID ADE03979 standard; cDNA; 1 DE Human PRO polynucleotide # PN US2003199057-A1. PP 23-OCT-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 50.85% Best Local Similarity: 35.15% Ouery Match: 061	6 standard uman secrei 94765-A1. 2003.	arity: milarity:	RESOLD 392 ID ADE22208 standard; cDNA; DE CDNA encoding human PRO p PN US2003199056-A1. PD 23-C7T-2003	GENENTECH arity: milarity:	TESCUL 393 ID ADD79432 standard; CDNA; 1295 BP DE CDNA encoding human PRO polypept PN US2003201428-A1.	GENENTECH arity: milarity:	KESULI 994 ID ADE41968 standard; cDNA;

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ADE33380 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
JS2003194767-A1.
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18333932 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003194791.Al.
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ADE34696 standard; cDNA; 1295 BP.
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(GETH ) GENENTECH INC.

Cent Similarity: 50.85$
Clocal Similarity: 35.15$
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ry Match: 26.42$
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Human PRO polynucleotide #168.
US2003199053-A1.
23-OCT-2003.
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Human PRO polynucleotide #168.
US2003194768-A1.
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cent Similarity: 50.85%
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24-APR-2003.  (GETH ) GENENTECH 1  Ent Similarity:  Coal Similarity:  Match:		KESULT 1004  ID ADE43085 standard; CDNA; DE Human PRO polynucleotide PN US2003199033-A1. PD 23-OCT-2003. PA (GETH ) GENENTECH INC. Percent Similarity; 50.885 Query Match: 25.155 Query Match: 25.425 RESULT 1005 ID ADD98674 standard; CDNA; DE: Human PRO polynucleotide PN US2003199059-A1.	PD 23-OCT-2003. PA (GETH) O GENENTECH INC. Percent Similarity: 50.88 Best Local Similarity: 35.119 Query Match: 26.44 RESULT 1006. ID ADE2760 standard; CDNA, DE CDNA enceding human PRO	23-OCT-2003. (GETH ) GENENTECH INC ent Similarity: 50 5. Local Similarity: 36 7. Match: 26	RESULT 1007  ID ADD78878 standard; CDNA; 1295 BP.  DE CDNA encoding human PRO polypeptide PN US2003203429-A1.  PD 30-OCT-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 50.85% CC  Best Local Similarity: 35.15% Mi	standard, an secret 766-Al. 03. ENENTECH rity: ilarity:	RESULT 1009  DE ADE42520 standard; CDNA; 1  DE Human PRO polynucleotide #  N US2003199032-A1.  PD 23-OCT-2003.  PA (GETH) GENEWTRCH INC.  Percent Similarity: 50.85%  Dest Local Similarity: 35.15%  Query Match: 26.42%  RESULT 1010  D ADD80536 standard; CDNA; 1  D CDNA encoding human PRO po  PR US2003207418-A1.  PO 6-NOV-2003.
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ADG21485 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207355-Al.
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Novel human secreted and transmembrane protein PRO245 CDNA.
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PA (GETH ) GENENTECH INC.

Percent Similarity: 50.85$ Co.

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Query Match: 26.42$ II

RESULT 1013

ID ADE04647 standard; CDNA; 1295 BP.

DE Human PRO polynucleotide #168.
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ADG80525 standard; CDNA; 1295 BP.
Human PRO polyrucleotide #168.
US2003207373-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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Human PRO polynucleotide #168.
US2003199031-A1.
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RESULT 1014
ID ADE92776 standard; CDNA; 1295 BP.
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Human PRO polynucleotide #168.
US2003207370-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 50.85%
Best Local Similarity: 35.15%
Query Match: 26.42%
RESULT 1011
ID ADD09564 standard; cDNA; 1295 BP
DE Human PRO polynucleotide #168.
PN US2003199028-A1.
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US2003194777-A1.
16-OCT-2003.
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PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
PACCENT Similarity: 50.85% Best Local Similarity: 26.42%
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PN 23-OCT-2003.

PA (GETH ) GENENTECH INC.

Percent Similarity: 50.85%

Best Local Similarity: 26.42%
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ID ADG23126 standard;
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RESULT 1012
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50.85% 35.15% 26.42%	; cDNA; 1295 BP. lectide #168. INC. 50.85\$ 25.42\$	cDNA, 1295 BP encoding PRO245	35.15%	cDNA; 1295 BP. smembrane prote	INC. 50.85% 35.15% 26.42%	cDNA; 1295 BP. d and transmembrane		cDNA; 1295 BP. d and transmem	INC. 50.85% 35.15% 26.42%	cDNA; 1295 BP. smembrane prote	INC. 50.85% 35.15% 26.42%		INC. 50.85\$ 35.15\$ 26.42\$
rity: ilarity:	standard O polynuc. 7372-A1. 003. GENENTECH arity: milarity:	DN,	Best Local Similarity: Query Match: RESULT 1021	ID ADH59179 standard; CDNA; 1295 BP. DE Human secreted/transmembrane protein CDNA, PN US200303972-A1.	PA (GETH ) GENENTECH II Percent Similarity: Best Local Similarity: Query March:	DE ADH55265 standard; DE Novel human secrete: PN US2003207381-A1.	PD 06-NOV-2003.  PAA (GETH) GENENTECH INC. Percent Similarity: 50.85% Best Local Similarity: 35.15% Query Match: 26.42% RESULT 1023	ID ADH55817 standard; cDNA; 1:0 DE Novel human secreted and t: PN US2003207379-A1.	PD 06-NOV-2003. PA (GETH) GENENTECH II Percent Similarity: Best Local Similarity: Query Match:	ID ADI37958 standard; cDNA; 1295 BP. 'DE Human secreted/transmembrane protein PN US200305435-A1.	PA (GETH ) GENENTECH II Percent Similarity: Best Local Similarity: Query Match:	ADI64036 standard; Novel human secrete US2003207385-A1.	PD 06-NOV-2003.  PD 06-NOV-2003.  Percent Similarity: Best Local Similarity: Query Macch: RESHIT 1026

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ACCEPTOR ACCEPTOR STANDA, 1295 BP.

DB ACCEPTOR Human secreted and transmembrane protein PRO245 CDNA.

BN US2003032156-A1.

PD 13-FEB-2003.

PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Percent Similarity: 50.85 Mismatches: 128

GUERY Match: 26.42$ Indels: 16

RESULT 1032

DD ACASB345 standard; CDNA, 1295 BP.

DE CDNA encoding human PRO polypeptide #11.

PN US2002192659-A1.

PD 19-DEC-2002.

PA (GETH) GENENTECH INC.

PA (GETH) GENEN
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7L 1027
AD163484 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207387-A1.
06-NOV-2003.
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t Local Similarity: 35.15$ Mismatches: 128
ry Match: 26.42$ Indels: 16
ULT 1028
ADH81898 standard; CDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 CDNA.
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ADH81346 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
05-NOV-2003.
ADI64985 standard; cDNa; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207386-A1.
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ADJ26226 standard; cDNA; 1295 BP.
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# US2002146709-A1.

# US2002146709-A1.

# GETH | GENENTECH INC.

# SEL Local Similarity: 35.158

# MATCh:

# ACASS948 standard Similarity: 26.428
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(GETH ) GENENTECH INC.

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Al. TTECH INC. :: 50.85% :ity: 35.15% dard; cDNA; 1295 BP gard; cDNA; 1295 Al.	TECH INC. 1: 50.85\$ 1: 50.85\$ 1:ty: 35.15\$ 26.42\$ idard; CDNA; 1295 BP ynucleotide #168.	30-COL-2003.  int Similarity: 50.85\$  Local Similarity: 35.15\$  Mistyres 26.42\$  ADE79565 standard; CDNA; 1295 BP.  Human secreted/transmembrane protein	INC. 35.15% 26.42% ; CDNA; 1295 B		(GETH ) GENENTECH INC.  201 Similarity: 50.85% Co Local Similarity: 35.15% Mi Ly Match: 26.42% In LY 1048  ADE22312 standard; CDNA; 1295 BP.  CDNA encoding human PRO polypeptide US2030922108-A1.	GETH ) GENENTECH INC.  Inc Similarity: 50.85% Cc. Local Similarity: 35.15% Mixeh:  Anten: 26.42% If ADE33864 standard; CDNA; 1295 BP.  US2003092110-A1.	15-GGTH ) GENENTECH INC.  OC Similarity: 50.85% CC Local Similarity: 35.15% Mi Match: 26.42% Ir T 1050 ADE24507 standard; CDNA; 1295 BP.  CDNA encoding human PRO polypeptide US2003092111-A1.
PN US2003100087-A1. PD 29-MAY-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 50.053 Rest Local Similarity: 35.15 Query Match: 26.423 ID ADD87884 standard; CDNA; DE Human PRO Polyuncleotide PN US2003092113-A1.	g # Kg	g # £ Ę	CONTROLLE AND A CONTROLL AND A CONTROLL AND A CONTROLL SIMILATICY: 50.85% Best Local Similarity: 50.85% Ouery Match: 26.42% Ouery Match 13.42% Ouery Match 13.	Siry at Co	g # £E	PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match: RESULT 1049 ID ADE23864 standard; DE CDNA encoding hum PN US2003092110-A1.	PA (GETH ) GENERTECH Percent Similarity: Best Local Similarity: Best Local Similarity: Query Match: RESULT 1050 ID ADE24507 standard DE CDNA encoding hum PN US2003092111-A1.
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46 128 16	46 128 16	46 128 16	46 128 16	46 1128 16	PRO245 CDNA. 46 128 16	46 128 16 PRO245 CDNA.	46 128 16
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ope ope	cDNA, 1295 BP. in PRO polypeptide INC. 50.85\$ 35.15\$ III	cotide #168. lectide #168. INC. 50.85\$ 26.42\$	CDNA, 1295 BP. In PRO polypeptide LivC. 50.85\$ 35.15\$ M 26.42\$ III	CDNA; 1295 BP. nsmembrane protein INC. 50.85\$ Co 35.15\$ Mii	cd and transmembrane ed and transmembrane INC. 50.85\$ Cons. 35.15\$ Mism.	cotide #168.  INC. 50.85\$ Mism. 26.42\$ Inde. cDNA; 1295 BP.	INC. 50.85% Con 35.15% Mii 26.42% In CDNA; 1295 BP. unsmembrane protein INC.
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rce st ery SUL	ID ADI DE CDD DN USX PD 23: PA (GR Percent Best Loc Query M	ID AND TO THE PROPERTY METERS OF THE PROPERTY	ID ADD ID ADD PN US; PD 23 PD 23 PA (GF Percent Best Loc	RESULT 1  1D ADIS  DE HUU  PN US;  PD 13- PA (GF  PA (GF  PA (GF  PETCENT MS  DEST LOC	ID AD	About the control of	PD 23-001 PD 23-007 PA (GETH ) Percent Similar Series Local S Query Match: RESULT 1066 ID ADE9897 DE HUMAN S PN US20032 PD 13-NOV-PA (GETH )

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ID ADF98584 standard; CDNA; 1295 BP.	Uc-NOV-ZUU3.  (GETH) GENEWECH cent Similarity: tt Local Similarity: tt Local Similarity: tt Lovar Natch: ADF99136 standard Human PRO polymuc. US2003207353-A1. 06-NOV-2003.	PA (GETH ) GENENTECH INC.  Percent Similarity: 50.85\$ Conservative: 46  Best Local Similarity: 35.15\$ Mismacches: 128  Query Match: 26.42\$ Indels: 16  RESULT 1077  ID ADG16721 standard; CDNA; 1295 BP.  DE CDNA encoding human PRO polypeptide #168.	PA GENOV-2003.  PA GENOV-2003.  PA GENOV-2003.  Percent Similarity: 50.85\$ Conservative: 46  Best Local Similarity: 35.15\$ Mismacches: 128  Query Match: 26.42\$ Indel8: 16  RESULT 1078  DE Human PRO polynucleotide #168.  PN US200320735+A1.	C m m m	2 4 4 5	Percent Similarity: 50.85\$ Conservative: 46 Best Local Similarity: 35.15\$ Mismatches: 128 Query Match: 26.42\$ Indels: 16 RESULT 108 DE CDNA encoding human PRO polypeptide #168. Pip 06.NOV-200357-A1.	PA (GETH) GENERATECH INC.  PA (GETH) GENERATECH INC.  Percent Similarity: 50.85\$ Conservative: 46  Best Local Similarity: 35.15\$ Mismatches: 128  Query Match: 26.42\$ Indels: 16  RESULT 1082  ID ADG08341 standard; CDNA; 1295 BP.
46 128 16	128 16	46 128 16	46 128 16 PRO245 CDNA.	46 128 16	16 128 16	46 128 16 PRO245 CDNA.	46 128 16 .
tive: es: #13.	Bervative: matches: lels: CDNA, #13.	uservative: matches:  els:	Conservative: Mismatches: Indels: 1295 BP. transemebrane protein PR	vative: ches: :	Conservative: Mismatches: Indels: BP.	Conservative: Mismatches: Indels: mbrane protein	Conservative: Mismatches: Indels:
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US2003207356-A1.
   Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207424-A1.
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RESULT 1088
ID ADG24868 standard; CDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 CDNA.
PN US2003207427-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
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Novel human secreted and transmembrane protein PRO245 cDNA.
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Novel human secreted and transmembrane protein PRO245
US2003207389-Al.
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ADG15511 standard, CDNA, 1295 BP.
CDNA encoding human PRO polypeptide #168.
US2003219885-A1.
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US2003207374-A1.
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Human PRO polynucleotide #168.
US2003207371-A1.
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US2003207423-A1.
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PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 50.85$
Best Local Similarity: 35.15$
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PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENEWTECH INC.
Percent Similarity: 50.85%
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PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 50.88
Best Local Similarity: 35.11
RESULT 1090
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                       DE CDNA encoding human PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH IN Percent Similarity: 3 Best Local Similarity: 3
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ADG06094 standard;
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ADG55764 standard; cDNA; 1295 BP. Novel human secreted and transmembrane protein PRO245 cDNA. US2003207365-A1.
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Novel human secreted and transmembrane protein PRO245 CDNA.
US2003207390-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207428-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207364-Al.
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US2003207362-A1.
                                                                                      ADGS5212 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245
US2003194778-Al.
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Human secreted/transmembrane protein cDNA, #13
US2003027145-A1.
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Human PRO polynucleotide #168.
US2003207358-A1.
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PD 16-OCT-2003.
PC (GETH) GENENTECH INC.
Percent Similarity: 50.85%
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PD 06-TH ) GENENTECH INC.
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PD 06-NOV-2003.

PA (GETH ) GENENTECH
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<b>=</b>	ADG58524 standard; cDNA; Novel human secreted and US2003207368-A1.	PA (GETH) GENERTECH Percent Similarity: Best Local Similarity: Query Match:	KESULI 1100 ID ADG70890 standard; DE Novel human secreti	<b>x</b>	nr 1101 ADG92586 standard; cDNA; 1295 BP. Human secreted/transmembrane protein cDNA,	US2003027146-A1. 06-FEB-2003. (GETH ) GENENTECH nt Similarity: Local Similarity: Match:	T 1102 ADG57972 standard; cDNA; Novel human secreted and US2003207363-Al.	2003. GENENTECH larity: imilarity:	ADG53556 standard; cDNA; Novel human secreted and US2003207415-A1.	PA GETH JENNY-2003. PA (GETH JENNY-ECH JENNY-ECH SIMILATILY: Best Local Similarity: Query Match:	ADG71442 standard; cDNA; Novel human secreted and US2003207421-A1.	/-Z003. ) GENENTECH nilarity: Similarity:	KESULT 1105 ID ADG81629 standard; CDNA; DE Human PRO polynucleotide PN US2003207985-A1.	nilarity: Similarity: 1:	ADHJ0591 standard; cDNA; Human PRO polynucleotide US2003077723-A1. 24 APR-2003. (GETH ) GENENTECH INC.
PD 06-NOV-2003. PA (GETH ) GENENTEC Percent Similarity. Best Local Similarity Query March:	AESOLI 1039 ID ADGS8524 8t DE NOVEL human PN US200320736 PD 06-NOV-2003	PA (GETH) Percent Simi Best Local S Query Match:	ID ADG708	ng St.	RESULT 1101 ID ADG925 DE Human	PN US2003027146-A1. PD 06-FEB-2003. PA (GETH ) GENENTEC PERCENT SIMILARILY: BEST LOCAL SIMILARILY: Query MATCH:	RESULT 1102 ID ADG579 DE Novel	PD 06-NOV-2003. PA (GETH ) GENENTEC Percent Similarity: Best Local Similarity Query Match:	RESULT 1103 ID ADG535 DE Novel PN US2003	PA (GETH ) Percent Simil Best Local Signery Match:	ID ADG714 DE Novel PN US2003	PA (GETH ) GENENTEC Percent Similarity: Best Local Similarity Query Match:	KESULT 1105  1D ADG816  DE Human  PN US2003	Percent Similarity: Best Local Similarity Query Match:	ID ADH30591 8th DE Human PRO p PN US200307772 PD 24-APR-2003

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Ouery Match:	standard; man secret 7367-A1.	06-NOV-2003. (GETH ) GENENTECH nt Similarity: Local Similarity: Match:	RESULT 1116 ID ADG59700 standard; CDNA; DE Novel human secreted and PN US2003207369-A1. PD 06-NOV-2003	(GETH) GENENTECH the Similarity: local Similarity: Match:	7 1117 ADH20375 standard; Human secreted/tra	PA (GETH ) GENENTECH INC. Percent Similarity: 50.85% Best Local Similarity: 35.15% Query Match:	ADH07230 standard; cDNA; 1295 BP. Human secreted/transmembrane protein cDNA. US200406511-A1.	B-JAN-2004. DESN/) DESNOYERS GODD/) GODDARD A. GODO/) GODOWSKI P. GIRN/) GIRNEY A.	MATH/) MATHER J P WILL/) WILLIAMS P WOOD/) WOOD W I	nt Similarity: local Similarity: Match:	Jr 1119 ADM5975 standard; cDNA; 1295 Human secreted/transmembrane US2003215904-A1.	PD 20-NOV-2003. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Ouery Match:	T 1120 ADH06803 standard; CDNA; 1295 BP Human secreted/transmembrane pro US2004005665-Al	PD 08-JAN-2004. PA (DESN/) DESNOYERS L. PA (GODD/) GODDARD A. PA (GODD/) GODDARD P. PA (GURN/) GURNEY A L.	PA (WATH) MATHER J P PA (WILL/) WILLIAMS P PA (WOOD/) WOOD W I. Percent Similarity: Query Match: TESUIT 1121	ADIBIL24 standard; cDNA; cDNA encoding human PRO
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(15338 standard; cDNA; 1295 BP.

fel human secreted and transmembrane protein PRO245 CDNA.
2003207382-A1.

NOV-2003.

SIMILARITY: 50.85$ CONSERVATIVE: 46

SIMILARITY: 50.85$ Mismatches: 128

ALCH:
26.42$ Indels: 16
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MDI1829: MD
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Human sected/transmembrane protein CDNA, #13.
Human sected/transmembrane protein CDNA, #13.
US200148419-A1.
07-AUG-2003.
(GETH ) GENENTECH INC.
CGETH ) CONSERVATIVE:
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nan secreted/transmembrane protein cDNA, #13.
003190610-A1.
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2003096340-A1.
MAY-2003.
ETH ) GENENTECH INC.
Similarity: 50.85$ Conservative: 28. Mismatches: 26.42$ Indels:
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ETH ) GENENTECH INC.

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(GETH ) GENENTECH INC.
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mindels: 16  P. Conservative: 46 Mismatches: 128 Indels: 16 Mismatches: 128 Indels: 16 Mismatches: 16 Conservative: 46 Mismatches: 16 Mismatches: 16 Conservative: 46 Mismatches: 16 Misma	transmembrane protein PR0245  transmembrane protein PR0245  Conservative: 46 Mismatches: 128 Indels: 16  Conservative: 46 Mismatches: 16  L295 BP.  Conservative: 46 Mismatches: 16  L295 BP.  Conservative: 46 Mismatches: 16  Indels: 16  Conservative: 46 Mismatches: 16  Indels: 16  L295 BP.	ID ADM29776 DE Human se PN US200319	PD 09-0CT-2 PA (GET) PA (GET) Percent Simil Best Local Si	ESULT 138 RESULT 1138 ID ADJ77441 DE Human PR PN US200403	ű t	Dest Doct of Match:  RESULT 1139  ID AD465563	Ü	Best Local Si Query Match: RESHIT 1140	ID ADM27699	PN US200404	ဗ္ဗ	Best Local Si Query Match:	RESULT 1141 ID ADM42423	PA (GETH ) Percent Simil	Best Local Si Query Match:	RESULT 1142 ID AD006098	DE Human PR	Percent Simil	Best Local Si Ouery Match:	RESULT 1143 ID ADN35291		-	PA (GETH ).   Percent Simil	Best Local Si Query Match:	RESULT 1144 ID ADM28285	DE CDNA enc PN US200407	PA CGETH )  PA (GETH )  Description	יייייייייייייייייייייייייייייייייייייי
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ADM29776 standard, Human secreted (true US2003190511-A1.  US2003190511-A1.  GETH ) GENENTECH Cent Similarity: FY MATCH: US200403336-A1. CS-FEB-2004.  GETH ) GENENTECH CENT Similarity: FY MATCH: US200403336-A1. CGETH ) GENENTECH CONA encoding huma US200403335-A1. CGETH ) GENENTECH C	CDNA; 1295 BP. nsmembrane prot INC.	5.15	cDNA; 1295 B eotide #168.	INC. 50.85%	25.13% 26.42%	PRO	5	.85	26.42	CDNA; 1	INC.	50.85%	26.42%	CDNA	2	INC.	50.85% 35.15%	26.42%	CDNA; 1295 B	÷	INC.	여.	26.4	DNA; 1295 B		INC 50	35.15% 26.42%		cDNA; 1295 BP. n PRO polypepti	IN	50.85% 35.15% 26.42%	.72°.
	ADM29776 standard; Human secreted/tra US2003190611-A1. 09-OCT-2003.	115 Ca	M77441 standard; man PRO polynucl 2004038336-A1. -FEB-2004.	GENENTECH		sta odin	B-2004.		•	stand oding	11-MAR-2004. (GETH ) GENENTECH	ent Similarity: Local Similarity:		3 stand	US2004058424-A1.	STH ) GENENTECH	larity: imilarity:		98 standard;	US6686451-B1.	STH ) GENENTECH	imilarity:		ADN35291 standard; Human PRO245 gene.	WO2004031105-A2. 15-APR-2004.	ETH ). GENENTECH Similarity:	imilarity	ULT 1144	ADM28285 standard; cDNA encoding humar US2004077064-A1	-APR-2004. ETH ) GENENTECH	nt Similarity: Local Similarity: Match:	raccii: I 1145 ADR10950 standard;

Mismatches: Indels:

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Query Match: 25.87% Indels: 11
RESULT 1154
DB AAF74414 standard; DNA; 905 BP.
DB Anglogenesis protein AAAl nucleotide sequence (Fig 7)
PN WO200111086-A2.
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cDNA DNA35638 encoding A33 related antigen PRO245.
WO9927098-A2.
                                            ADS74498 standard; CDNA; 1295 BP.
Human secreted/transmembrane cDNA #13.
US2004185531-A1.
23-SEP-2004.
(ASHK) ASHKENAZI A.
(BOTS/) BOTSTEIN D.
(DESN/) DESNOYERS I.
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RESULT 1153
ID AA161103 standard; cDNA; 930 BP.
DE Human polynucleotide SEQ ID NO 5092.
PN WO200153312-Al.
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RESULT 1156
ID AAX56523 standard; DNA; 396 BP.
DE Human T84016 DNA fragment.
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PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 56.11%
Best Local Similarity: 39.37%
Query Match: 25.62%
RESULT 1155
ID AAX37717 standard; DNN; 297 BP.
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PA (HYSE-) HYSEQ INC.
Percent Similarity: 55.75%
Percent Similarity: 55.75%
Percent Similarity: 25.87%
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Query Match: 26.30%
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PA (GETH ) GENENTECH INC.

Percent Similarity: 81.

Best Local Similarity: 81.
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WILLIAMS P M.
WOOD W I.
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DESNOYERS L.
EATON D L.
FERRARA N.
FILVAROFF E.
                                                                                                                                                                                                                                                                                                              GODOWSKI P J. GRIMALDI C J.
                                                                                                                                                                                                                                                                                                                                                                              KLJAVIN I J.
MATHER J P.
PAN J.
PAONI N F.
ROY M A.
STEWART T A.
                                                                                                                                                                                                                                                                                                                                                GURNEY A L.
HILLAN K J.
   Sest Local Similarity:
                                                                                                                                                                                                                                                                                              GODDARD A.
                                                                                                                                                                                                                                                   GERBER H.
                                                                                                                                                                                                                          FONG S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TUMA/)
(WILL/)
(WOOD/)
                     Query Match:
RESULT 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                   (PAON/)
(ROYM/)
(STEW/)
                                                                                                                                                                         (EATO/)
(FERR/)
(FILV/)
                                                                                                                                                                                                                                                                                                                                                                                (KLJA/)
(MATH/)
(PANJ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match:
                                                                                                                                                                                                                                                            (GERB/)
(GERR/)
                                                                                                                                                                                                                                                                                                                              (GRIM/)
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Query
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ID A
DE C
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DE CDNA enc.

NUSSO03077659-r.

PN US20032077659-r.

PA (GETH ) GENENTECH INC.

Percent Similarity: 50.85$ Mismatch.

Query Match: 26.42$ Mismatch.

RESULT 1148

ID AD196319 standard, CDNA, 1295 BP.

DE Novel human secreted and transmembrane protein PRO245 CDNA.

US2003207354-A1.

"NV-2003.

"NV-2003.

"NFMTECH INC.

Source A6

Mismatches: 128

Indels: 16
                                                                       46
128
16
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128
16
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DE Human secreted/transmembrane protein cDNA, #13.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 50.85$ Conservative: 4
Best Local Similarity: 35.15$ Mismatches: 1
Query Match: 26.42$ Indels: 1
RESULT 1146
ID ADRI7859 standard; CDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004147017-A1.
                                                                     Conservative:
Mismatches:
Indels:
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Mismatches:
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Mismatches:
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ID ADT03535 standard; CDNA; 1295 BP.
DE Human secreted/transmembrane protein CDNA, #13.
PN US2003152922-A1.
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Human PRO245 cDNA sequence.
AU2003259607-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID ADT94236 standard; CDNA; 125
DE Human PRO245 CDNA sequence.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 50.85%
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35.15%
26.42%
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35.15%
26.42%
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PD 14-AUG-2003
PA (GETH ) GENETTECH INC. PARCELL Similarity: 50.8F Best Local Similarity: 35.1E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAN J.
PAONI N F.
STEWART T A.
TUWAS D.
WILLIAMS P M.
                                                                                                                                                                                                                                                                                                                                              GERBER H.
GERRITSEN M E.
                                                                                                                                                                                                                                                                                                                                                                                  GODDARD A.
GODOWSKI P J.
GRIMALDI C J.
                                                                                                                                                                                                         ASHKENAZI A.
BOTSTEIN D.
DESNOYERS L.
                                                                                                                                                                                                                                                                                                                                                                                                                                   GURNEY A L.
HILLAN K J.
KLJAVIN I J.
                                                                                                                                   DE Human secreted/transi

DE Human secreted/transi

PA (ASHK) ASHKENAZI A.

PA (ASHK) ASHKENAZI A.

PA (BOTS/) BOTSTEIN D.

PA (BOTS/) BOTSTEIN D.

PA (EATO/) EATON D L.

PA (FERR/) FERRARA N.

PA (FONG/) FONG S.

PA (GAOW) GAO W.

PA (GERR) GERRITSEN M.

PA (GERR) GERRITSEN M.

PA (GERR) GERRITSEN M.

PA (GEND/) GODDREN P.

PA (HILL/) HILLAN J.

PA (HILL/) HILLAN J.

PA (HILL/) PAN I.

PA (HILL/) PAN I.

PA (RUJA/) KLJAVIN I J.

PA (RUJA/) KLJAVIN I J.

PA (RUJA/) TUMAS D.

PA (RUJA/) TUMAS D.

PA (WODD/) WOOD W I.

PECCENT SITMLIANS P.

PA (WODD/) WOOD W I.

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PA (WOOD/) WOOD W I.
                                                                                                                                                                                                                                                                                            FILVAROFF E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MATHER J P.
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46 128 16

Conservative: Mismatches: Indels:

46 128 16

Conservative: Mismatches: Indels:

39 89

Conservative: Mismatches: Indels:

0 18

Conservative: Mismatches: Indels:

37 86 11

Conservative: Mismatches: Indels:

14 22 22

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cDNA; 1430 BP.
human diagnostic protein #22332.
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US2003077606-Al.
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RESULT 1166
ID ABV83958 standard; CDNA; 367 BP
DB Human polynucleotide SEQ ID NO 324.
PN US2002090672-A1.
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                                                                                                                                                                           ABA06658 standard; cDNA; 367 BP.
Human cDNA SEQ ID NO: 324.
WO200154474-A2.
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ID ADB31520 standard; CDNA; 367 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA; 252 BP.
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                                                                                                                                                                                                                                         PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 79.65%
Best Local Similarity: 67.26%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PA (HTVA-) HTVAN GENOME SCI INC. Percent Similarity: 79.65%
Best Local Similarity: 67.26%
Query Match: 23.61%
                                 02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
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Cent Similarity: 100.00$
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PD 25.MAR-1999.
PA (GETH) GENENECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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Human 2252527 DNA fragment.
WO9914241-A2.
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PD 11-OCT-2001.

PD 11-OCT-2001.

Percent Similarity: 48.44%

Best Local Similarity: 34.69%
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WO9914241-A2.
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AAXSESO9 standard; DNA; 25(
Human 2197534 DNA fragment
WO9914241-A2.
                                                                        Percent Similarity: 79.65%
Best Local Similarity: 67.26%
Query Match: 23.61%
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RESULT 1170
TD AAX56503 standard; D/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-2002.
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JLT 1169
AAS86528 standard; c
DNA encoding novel h
     WO200155320-A2.
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RESULT
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RESULT 1164
RD HALLO2302 standard; CDNA; 367 BP.
DE Human reproductive system related antigen CDNA SEQ ID NO: 2303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL51600 standard; DNA; 933 BP.
Human junctional adhesion molecule 3 (huJAM3) coding sequence.
WO20030008541-A2.
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Novel canine microarray-related DNA sequence SeqID4731
WO2004063324-A2.
                                                                                                                                                                                                                                                                                                       48
137
18
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Human immunoglobulin encoding cDNA SEQ ID No
WO200155315-A2.
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1D ABL3 980 BP.

DE Human NS cDNA sequence SEQ ID NO:1.

PN WO200206315-A2.

PD 24-AN-2002.

PA (COMP-) COMPUGEN LTD.

Percent Similarity: 49.02% CC
                                                                                                                                                                             AAA95305 standard; cDNA; 1626 BP.
                                                                                                                                                                                          DE Murine CRAM-2 coding sequence.
PN W0200053749-A2.
PD 14-SEP-2000.
PA (RMPD-) RMP DICTAGENE SA.
Percent Similarity: 49.18%
Best Local Similarity: 33.44%
Query Match: 25.32%
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Human 1508565 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                   JT 1158
AAX37720 standard; DNA; 220 BP.
Human clone 1508565 DNA.
WO9914241-A2.
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PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 79 65%
Best Local Similarity: 67.26%
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PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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25.06%
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PA (ELIL) LILLY & CO ELI.

PACEOUT Similarity: 47.90%

Best Local Similarity: 32.69%

Onorw Match: 24.87%
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37.91%
23.67%
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80.17$
25.45$
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PA (GENE-) GENE LOGIC INC.
PA (PFIZ ) PFIZER PROD INC.
Percent Similarity: 54.98#
Best Local Similarity: 37.91#
Query Match: 23.67#
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Query Match: 24.94%
PN W09914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 80.17
Query Match: 3milarity: 80.17
Query Match: 1157
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PA (GETH ) GENENTECH INC.
Percent Similarity: 100
Best Local Similarity: 100
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222

222

44 134 31

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AAK93247 standard; cDNA; 824 BP.
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RESULT 1182
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RESULT 1181
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RESULT 1185
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WO2004053058-A2.
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109
69
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Human cDNA 5'-end sequence, SEQ ID NO: 813
EP1130094-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADG39448 standard; cDNA; 714 BP.
Human JAM-2 encoding cDNA SEQ ID NO:17.
WO2003104400-A2.
DE ..
PN EP14*.
PD 28-JUL-20.
PP 28-JUL-20.
PP 28-JUL-20.
Percent Similarity: 28...
Query Match: 22.77$
RESULT 1173
ID AAX56507 standard; DNA; 257 BP.
Human 1299110 DNA fragment.
"19914241-A2.
"Re-1999."
"Re-1999."
"Re-1999."
"Re-1999."
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RESULT 1176
ID ADP56688 standard; CDNA; 798 BP.
                                                                                                                                                                                                                                                                                                                                                                                    Query Match: 21.76*
RESULT 1175
ID AAXS6513 standard; DNA; 257 BP. DE Human 492141 DNA fragment.
PN W09914241-A2.
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                                                                                                                                                                                                                                                                             AAX56527 standard; DNA; 191 BP.
Human 1508552 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D ADP5668 standard; cura, constitution adhesion molecular My02004053058-A2.

PD 24-JUN-2004.

PA (ELIL) LILLY & CO ELI.

Percent Similarity: 48.10%

Best Local Similarity: 32.91%
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PD 23-OCT-2003.
PA (RMFD-) RMF DICTAGENE SA.
Percent Similarity: 48.31%
Best Local Similarity: 33.05%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PN WO2003104400-A2.
PD 18-DEC-2003.
PA (RMFD-) RMF DICTAGENE SA.
PA (UYPE-) UNIV PENNSYLVANIA.
Percent Similarity: 48.31%
Best Local Similarity: 33.05%
Query Match:
RESULT 1179.
                                                                                                                                                                                                                                                                                                         PN W09914241-A2.
PD 25-MAR-1999.
PP (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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PA (HELL-) HELIX RES INST.
Percent Similarity: 45.454
Best Local Similarity: 31.274
Query Match: 21.057
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PA (GETH ) GENENTECH INC.

Percent Similarity: 90.

Best Local Similarity: 90.
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RESULT 1177
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RESULT 1178
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ADP69997 standard; cDNA; 618 BP.
Human NOV2a mature extracellular domain encoding cDNA SEQ ID NO:67.
WO2004055158-A2.
Human cDNA clone representative sequence, SEQ ID NO: 1707.
EP1130094-A2.
                                                                                                                                                                                                                                                                        5' end of a representative human cDNA cluster SeqID 1707.
EP1396543-A2.
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119
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Mismatches:
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5' end of a human cDNA molecule SegID 813
EP1396543-A2.
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WO2004055158-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAIS9317 standard; cDNA; 561 BP.
Human polynucleotide SEQ ID NO 1520.
WO200153312-A1.
                                                                                                                                                                                                                                                                                             PN PLOUGH PNAR-2004.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 45.45$
Best Local Similarity: 31.27$
Query Match: 21.05$
RESULT 1183
ID AAX56506 standard; DNA; 259 BP.
DE Human 3234064 DNA fragment.
PN W09914241.A2.
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PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 45.45%
Best Local Similarity: 31.27%
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RESULT 1188
ID AAX56501 standard; DNA; 303 BP.
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PA (HYSE-) HYSEQ INC.
Percent Similarity: 57.93%
Best Local Similarity: 20.11%
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31.27$
21.05$
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98.51%
20.66%
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Percent Similarity: 51.27%
Best Local Similarity: 34.01%
Ouery Match: 19.75%
                                        PA (HELL-) HELLY RES INST.
Percent Similarity: 45.4
Best Local Similarity: 31.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PA (GETH ) GENERATECH INC.
Percent Similarity: 98.
Best Local Similarity: 98.
Query Match: 20.
                            05-SEP-2001
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AAX37665 standard; cDNA; 413 BP.
Human PRO protein derived EST consensus sequence DNA30954.
WO9914241-A2.
                                                                                                                                                                                                                                                                                          Consensus sequence expressed sequence tag, EST, DNA30954.
US2002182206-A1.
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Mismatches:
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Human PRO245 consensus DNA fragment DNA30954.
WO2004031105-A2.
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ADA10946 standard; cDNA; 1556 BP
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Human 777818 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                              ADH62554 standard; DNA; 413 BP.
Human DNA30954 consensus DNA.
                                                                                                                                                                                                                                                                                CDNA; 413
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PD 15-APR-2004.
PD 16-TH J GENENTECH INC.
Percent Similarity: 58.91%
Best Local Similarity: 47.29%
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PD 25-MAR-1999.

PA (GETH) GENENTECH INC.
Percent Similarity: 83.82%

Best Local Similarity: 82.35%
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47.29%
17.91%
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Best Local Similarity: 47.29%
Query Match: 17.91%
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PA (GETH) GENENTECH INC.
Percent Similarity: 58.
                              03-JUN-1999.
(GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                              05-DEC-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ASHK/) ASHKENAZI A.
(FONG/) FONG S.
(GODD/) GODDARD A.
(GURN/) GURNEY A L.
(RAPI/) NAPIER M A.
(TUMA/) TUMAS D.
(WOOD/) WOOD W I.
                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                              ABX93489 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LASE/) LASEK A W. (JONE/) JONES D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity:
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                                                           Percent Similarity:
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               WO9927098-A2.
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RESULT 1199
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RESULT 1197
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RESULT 1196
ID AAX81783 standard; DNA; 413 BP.
DE Consensus sequence DNA30954 encoding an A33 related antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1191

ID ADP56687 standard; CDNA, 690 BP.

ID Human junction adhesion molecule 3 splice variant 1

DE Human junction adhesion molecule 3 splice variant 1

DE 4-JUN-2004.

PA (ELIL) LILLY & CO ELI.

PA (ELIL) LILLY & 48.43 Conservative: 35

Percent Similarity: 48.43 Mismatches: 100

LOCAL Similarity: 18.91 Indels: 15
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DNA encoding novel human diagnostic protein #22392.
W0200175067-A2.
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DE WO95.
PN WO95.
PD 25-MAR.15.
PA (GETH ) GENEN.
Percent Similarity:
Best Local Similarity: 90.1.
Query Match:
RESULT 1189
ID AAX56511 standard; DNA; 227 BP.
Human AA227408 DNA fragment.
"O9914241-A2.
"R-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT62383 standard; DNA; 2202 BP.
Mouse A33 antigen.
WO9708189-A1.
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PA (LUDW-) LUDWIG INST CANCER RES.

Percent Similarity: 47.35%

Best Local Similarity: 29.55%
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ID AAXS5608 standard; DNA; 243 BP.
DE Human AA101519 DNA fragment.
PN W09914241-A2.
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RESULT 1190
AAX56536 standard; DNA; 198 BP.
DE Human 1610836 DNA fragment.
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(GETH ) GENENTECH INC.
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PA (GETH) GENENTECH INC.

Percent Similarity: 93.

Best Local Similarity: 93.
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Percent Similarity: 94.
Best Local Similarity: 94.
Query Match: 18.
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Percent Similarity:
Best Local Similarity:
Query Match:
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(HYSE-) HYSEQ INC.
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P185
                 Human prostate tumour protein partial DNA sequence #131.
US2002090372-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH02556 standard; cDNA; 382 BP.
Prostate tumour antigen determined cDNA sequence for
WO200125272-A2.
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US2002192763-A1.
                                                                                                                                                                   ID AAH99491 standard; CDNA; 382 BP.

DE Human prostate-specific CDNA sequence P185.

PN WC200151633-A2.

PD 19-JUL-2001.

PA (CORI-) CORIXA CORP.

Percent Similarity: 100.00% Mismatche Coery Match: 16.39% Indels:
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Human prostate-specific cDNA sequence P185.
WO200134802-A2.
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Human prostate cDNA sequence #135.
WO200173032-A2.
      ABS71280 standard; cDNA; 382 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACA59392 standard; cDNA; 382 BP
ID ABS71280 standaru; c....,
DE Human prostate tumour protein
PN US2002090312-A1.
PD 11-UUL-2002.
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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(CORI-) CORIXA CORP.
int Similarity: 100.00%
Local Similarity: 100.00%
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Best Local Similarity: 100.00%
Query Match: 16.39%
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Best Local Similarity: 100.00%
Query Match: 16.39%
RESULT 1231
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OYT/) FOY T M.
Similarity: 100.00
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WANGA.
SKEIKYYA.W.
HEPLERWT.
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KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
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DILLON D C.
MITCHAM J L.
HARLOCKER S 1
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(CORI-) CORIXA CORP.
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RESULT 1228
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RESULT 1229
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RESULT 1232
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(WANG/
(SKEI/
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WO200004149-A2.
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cDNA sequence of prostate tumour clone.
WO9837093-A2.
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Prostate tumour specific gene clone.
WO9837418-A2.
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Human endothelial cell cDNA #5207.
US2003073623-Al.
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AAA06375 standard; cDNA; 382 BP.
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AAXS6537 standard; DNA; 237 BP.
Human 1274809 DNA fragment.
W09914241-A2.
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 PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 42.30%
Best Local Similarity: 25.57%
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DD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
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DD 27-ANG-1998.
PA (CORI-) CORIXA CORP.
Percent Similarity: 100.00%
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PA (CORI-) CORIXA CORP.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 16.39%
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PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
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PA (GETH ) GENENTECH INC.

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Best Local Similarity: 100.00$
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Query Match: 16.39%
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Human 1519947 DNA fragment
WO9914241-A2.
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Human 1521745 DNA fragment
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Best Local Similarity: 37.18%
Query Match: 16.45%
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(LABA/) LABAT I.
(STAC/) STACHE-CRAIN B.
(DICK/) DICKSON M C.
(JONE/) JONES L W.
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PA (CORI-) CORIXA CORP.
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RESULT 1227
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Best Local Similarity: 100 Query Match: 15 RESULT 1233 ID AAS10114 standard; cDP B Human prostate tumour PN 17-JUL-2001. PA (CORI,) CORIXA CORP. PAA (CORI,) CORIXA CORP. Best Local Similarity: 100 Best Local Similarity: 100 Guery Match: 16	5 standard, 185 cDNA se 22248-A1. 2002. XU J. DILLON D HARLOCKER JIANG Y. FALOS M D. FALOS M D. FATTER M P. STOLK J A. DAY C H. VEDVICK T CARTER D. STOLK J A. DAY C H. WENTER D. STOLK J A. DAY C H. WENTER D. SEINK Y F. WANG A. SKEIKY Y P. HEPLER W J.	MENULI 1255  DE Prostate tumour CDNA #135.  DE PROSTAGE tumour CDNA #135.  PN US2002081890-A1.  PA (XUJJ/) XU J.  PA (XUJJ/) XU J.  PA (DILL/) DILLON	89 stand prostate 128530-A 12083.0-A 11arity: Similariy: 05 stand 05 stand 05 contar 12009-A 12003.0- 11arity: Similariy:

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DNA encoding novel human diagnostic protein #22329. W0200175067-A2. [HT-OCT-2001. [HYSE-] HYSEO INC. nt Similarito
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Human PRO protein derived EST DNA sequence T89217.
WO9914241-A2.
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human diagnostic protein #4636.
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RESULT 1246

BESULT 1246

DE Human protein clone HP10568 full length coding to w020005357-A2.

PD 03-FEB-2000.

PA (SAGA) SAGAMI CHEM RES CENT.

PA (PROT-) PROFEGENE INC.

PA (PROT-) PROFEGENE INC.

PA (CROINDIAITLY: 29.33$ Mismatches:
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ID AAA18905 standard; CDNA, 981 BP.
ID Human protein clone HP10568 coding sequence. PN WO200005367-A2.
PD 03-FEB-2000.
PA (SAGA ) SAGAMI CHEM RES CENT.
PA (SAGA ) SAGAMI CHEM RES CENT.
PA (PROT-) FROTEGENE INC.
Percent Similarity: 43.73* Mismatches: Best Local Similarity: 29.39* Mismatches:
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                       D AASS6525 standard; CDNA; 493
DB DNA encoding novel human diagg
PN W0200175667-A2.
PD 11-0CT-2001.
PA (HYSE-) HYSEQ INC.
PECENT Similarity: 55.92%
Best Local Similarity: 16.35%
CDUETY MATCH: 16.35%
RESULT 1240
DE Human 956595 DNA fragment.
PN W09914241-A2.
PD 25-WAR-1999.
PA (GETH ) GENENTECH INC.
PERCENT Similarity: 100.00%
PERCENT Similarity: 100.00%
PECCAL Similarity: 15.74%
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DE Human PRO protein derive
PN W09914241-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
PA (GETH ) GENENTECH INC.
PA (GETH ) SIMILARITY; 61.86
Best Local Similarity: 48.45
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RESULT 1241

ID AA191738 standard; cl
DE Human polynuclectide
PN W0200164855-A2.
PD 07-28P-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 88
Query Match:
RESULT 1242
ID AAS68832 standard; cl
DE DNA encoding novel hy
PN W0200175067-A2.
PD 11-CCT-2001.
PA (HYSE-) HYSEQ INC.
PROCENT SIMILARITY: 50
PERCENT SIMILARITY: 50
PERCENT SIMILARITY: 50
PERCENT SIMILARITY: 50
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PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 5 Best Local Similarity: 3 Query Match: 1244
             RESULT 1239
ID AAS86525 standard;
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RESULT 1243
ID AAS76296 standard;
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,	131 standard; human secret 1088068-A1.	다 나무	1D AD873372 standard; of Novel human secreted PN US2003096968-AL. PD 22-MAY-2003.	ccent Similarity: st Local Similarity: sry Match: SULT 1257	DE ADD 0913-8 Edutadio, of DE Novel human secreted PN US2003092889-A1. PD 15-MAY-2003. DA (GETH ) GENERATOR IN	cent Similarity: it Local Similarity: rry Match: ULT 158		Percent Similarity: 2 Best Local Similarity: 2 Query Match: 1259 TRESULT 1259		g 7 7 5	1D ADS8 1/4 SEGRIGATO; OD THUMAN PRO polynuclec PN US2003088067-A1. PD 08 MAY-2003.	(GELT ) COMMENTED TO THE SIMILARITY: ST. LOCAL SIMILARITY: ST.Y MACCH: SULT 1261 ADB84856 Standard:		; ; ;	י ע.	PA (GETH ) GENENTECH IN Percent Similarity: 4 Best Local Similarity: 4 Query Match: 1263
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Query Match:	ij	PD 14-DEC-2000.  A (GETH) GENENTECH J PERCENT SIMILARILY: BEST LOCAL SIMILARILY: QUETY MATCH:	RESULT 1248 ID ABK33653 standard; CDNA; 1161 BP DE CDNA encoding human PRO protein, PN WO2000208288-A2. PD 31-7AN-2002	(GETH ) GENENTECH cent Similarity: st Local Similarity: sry Match:	ALSOLITATE TO ACAGE STANDARD, CDNA, 1161 BP.  DE Novel human secreted and transmembrane protein PRO7154 PN US2003088063-A1. PD OR-MAY-2003	(GETH ) GENENTECH cent Similarity: st Local Similarity: sry Match:	ID ABT44343 standard; DE Human PRO7154 cDNA. PN US2003050448-A1.	(GETH) GENERAL (GETH) GENERAL (Cent Similarity: st Local Similarity: sty Match:	2		KESULI 1232 ID AC08223 standard; CDNA; 116; DE Human secreted/transmembrane PN US2003044934-A1.	(GETH) GENENTECH ) cent Similarity: st Local Similarity: sry Match:	ID ABT43999 standard, cDNA; 1161 BP. DE Human membrane bound receptor/protein PR07154 PP US200165147-A1. PP 0.1-APR-2003	(GETH ) GENENTECH : ccent Similarity: st Local Similarity: sry Match:	ID ADB3725 standard; cDNA; DE Novel human secreted and PN US2003073814-A1.	PD 17-APK-2003. PA (GETH) GENENTECH 1 Percent Similarity: Best Local Similarity: Query Match:

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and transmembrane protein PRO7154 cDNA

DE Novel human secreted PN US2003096972-A1.	g # g g	cref 1.	£ 7 7 E	ID ADC77936 standard; cD DE Novel human secreted PN US2003088066-A1. PD 08-MAY-2003. PA (GETH ) GENEWIECH INC	ccent Similarity: st Local Similarity: ery Match: SULT 1274	DE Novel human secreted PN US2003105291-A1. PD 05-UN-2003	9 7 K	DE Novel human secreted PN US2003105290-A1. PD 05-JUN-2003.	iry UL	ADD50626 standard; Human PRO polynucl US2003096971-A1. 22-MAY-2003.	2 # 2 #	ADD50380 standard; Human PRO polynucl US2003096970-A1. 22-MAY-2003.	U 10 11 10	1D ADD2131 Standard; CD DE Novel human secreted PN US2003162289-A1. PD 05-JUN-2003.	PA (GETH ) GENENTECH INC Percent Similarity: 43 Best Local Similarity: 29 Query Match: 15 RESULT 1279 ID ACA66958 standard; CD
1161 BP. transmembrane protein PRO7154 cDNA.	Conservative: 40 Mismatches: 115 Indels: 42		Conservative: 40 Mismatches: 115 Indels: 42	·	Conservative: 40 Mismatches: 115 Indels: 42	1161 BP. transmembrane protein PRO7154 cDNA.	Conservative: 40 Mismatches: 115 Indels: 42	mbrane protein PRO7154 cDNA.	Conservative: 40 Mismatches: 115 Indels: 42	mbrane protein PF	Conservative: 40 Mismatches: 115 Indels: 42	1161 BP. transmembrane protein PRO7154 cDNA.	Conservative: 40 Mismatches: 115 Indels: 42	1161 BP. transmembrane protein PRO7154 cDNA.	Conservative: 40 Mismatches: 115 Indels: 42
ID ADB73126 standard; cDNA; 1161 BP DE Novel human secreted and transmer DN 11520023023.1	PD 15-MAY-2003.  PA (GETH ) GENEWECH INC.  Percent Similarity: 43.73%  Best Local Similarity: 29.39%  Query Match: 15.03%	D ALOGO 1161 BP DE Human PRO polynucleotide #118. PN US2003088065-Al. PD 08-MAY-2003.	PA (GETH ) GENENIECH INC. Percent Similarity: 43.73% Best Local Similarity: 29.39% Query Match: 15.03%	RESULT 1265 ID ADC21954 standard; cDNA; 1161 BP DE Human PRO polynucleotide #118. PN US2003096969-A1. PD 22-MAY-2003.	ir ce	5 standard; cDNA; 1man secreted and 88064-A1.	Ety F G	DE Novel human secreted and transmembrane protein PN US2003088070-A1.	PD 08-MAY-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 43.73%  Best Local Similarity: 29.39%  Query Match: 15.03%	andard; cDNA; secreted and L-A1.	PD 08-FAILZUGS. Percent Similarity: 43.73% Best Local Similarity: 29.39% Query Match: 15.03%	2 standard; cDNA; uman secreted and 88072-A1.	ir ce	cDNA; ed and	PD 05-JUN-2003.  PA (GETH ) GENENTECH INC.  Best Local Similarity: 29.39%  Query Match: 15.03%  RESULT 1271

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DNA; 1161 BP. and transmembrane protein PRO7154 cDNA.
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A1. TECH : ity:	ACD68710 standard; cDNA; Novel human secreted and US2003045687-A1.	TECH : ity:	Matcn: T.1281 ADC48938 standard; CDNA; Novel human secreted and	PN US2003092888-A1. PD 15-WAY-2003. PA (GETH ) GENENTECH INC. A3.73* Best Local Similarity: 43.73* Best Local Similarity: 29.39* Query Match:	T 1282 ADE21109 standard; cDNA; Novel human secreted and US2003100735-A1.	2003. GENENTECH larity: imilarity:	11 1263 ADE05953 standard; cDNA; Human PRO polynucleotide US2003100728-A1.	PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Ouery Match:	ID ADD75182 standard; cDNA; DE Human PRO polynucleotide PN HS2003100712-41	PD 29-MAY-2003.  PA (GETH ) GENENTECH INC. Percent Similarity: 43.73% Best Local Similarity: 29.39% Ouery March: 15.03%	AESOLI 1283 ID ADD75928 standard; cDNA; DE Novel human secreted and DN HS2003100717-A1	2003. GENENTECH larity: imilarity:	17 1286 ADD85160 standard; cDNA; Novel human secreted and US2003100722-A1.	TECH : ity:	ADD86986 standard; cDNA; Novel human secreted and US2003100738-Al.
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63 standard; cDNA; 1161 BP.
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100734-A1.
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096362-A1.
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100737-A1.
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Novel human secreted and transmembrane protein PRO7154 cDNA.
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ADD77962 standard; cDNA; 1161 BP.
Novel human secreted and transmembrane protein PRO7154 cDNA.
US2003100730-A1.
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RESULT 1306
ID ADD7716 standard; cDNA; 1161 BP.
DE NOVel human secreted and transmembrane protein PRO7154 cDNA.
PN US2003100729-Al.
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Novel human secreted and transmembrane protein PRO7154 cDNA.
US2003100716-A1.
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Novel human secreted and transmembrane protein PRO7154 cDNA.
US2003100731-A1.
29-MAY-2003.
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ID ADDB5420 standard; cDNA; 1161 BP.
DE Novel human secreted and transmembrane protein PRO7154 cDNA.
PN US2003100725-A1.
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Percent Similarity: 43.73$
Best Local Similarity: 29.39$
Query Match:
RESULT 1304
ID ADD86740 standard; cDNA; 1161 BP
DE Novel human secreted and transme
PN US2003100719-A1.
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RESULT 1309
ID ADD73952 standard; cDNA; 1161 BP
DE Human PRO polynucleotide #118.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
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RESULT 1310

ID ADD74690 standard; cDNA; 1161 BP

DE Human PRO polynucleotide #118.

PN US2003100713-A1.

PD 29-MAY-2003.

PA (GETH) GENENTECH INC.
                                                            ID ADD86740 standard; LLL., LDB Novel human secreted and tran US2003100719-A1.

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PA (GETH ) GENENTECH INC.

Percent Similarity: 43.73%

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RESULT 1311
ID ADD77218 standard; CDNA; 116
DE Novel human secreted and trapy US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
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PA (GETH ) GENENTECH INC.

Percent Similarity: 43.

Best Local Similarity: 29.
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RESULT 1305
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Query Match: RESULT 1320	1D AUG06/9/ DE Human PRO PN US2003096 PD 22-MAY-20	PA (GETH ) GI Percent Similar Best Local Sim Query Match: RESULT 1321	1D ADH39141 (DE NOVEL hum: DE NOVEL hum: DE 22-MAY-20(DE DE NOVEL HUM: ) CEPTIN (CEPTIN ) CEPTIN ) CEPTIN (CEPTIN ) CEPTIN (C	rce at Sg.	1D ADG34231 8 DE NOVEl hum: PN US20040AN-200 PD 08-JAN-200 PA (GETH ) GI	Str. 1	DE HUMAN PRO PN US2003096.	9 4 7 5	1D ADH69/95 6	rcent Simil st Local S: ery Match: SULT 1325	1D AD129356 B DE NOVE1 hum: PN US20030969 D	rcent Simi st Local S sry Match: SULT 1326	Novel hu US200404 04-MAR-2	PA (GETH ) GE PETCENT SIMILAN BEST LOCAL SIMILAN QUERY MATCH: RESULT 1327	DE Human PRO PN US20040441 PD 04-MAR-200 PA (GETH ) GF PETCENT Similan Best Local Similan Query Match:
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Query Match:	15.03%	Indels:	42
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5	CDNA; 1161 BP.		
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RESULT 1326 ID ADM27353 standard;	CDNA; 1161 BP.		
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PN US2004044179-A1. PD 04-MAR-2004.			
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	INC.		
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		Indels:	42

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ALSOBROOK J P.
ANDERSON D W.
BOLDOG F L.
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CASWAN S J.
CHAPOVAL A.
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(CURA-) CURAGEN CORP.
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PD 27-FEB-2004.
PA (GENE/) GENE S.
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(GORM/)
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DE Human signal peptide containing protein HSPP-28 cDNA SEQ ID NO:162.

PN WO200000610-A2.

PD 06-JAN-2000.

PA (INCY-) INCYTE PHARM INC.

Percent Similarity: 43.73% Conservative: 40

Best Local Similarity: 29.39% Mismatches: 115

Query Match: 15.03% Indels: 42

RESULT 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADF83096 standard; cDNA; 981 BP.
Human corticol thymocyte receptor CTXL, overexpressed in cancer.
WO2003100000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human diagnostic and therapeutic polynucleotide SEQ ID NO:2386 WO2004023973-A2.
                                                                                                                                            JT 1329
AAC98064 standard; cDNA; 1186 BP.
Human colon cancer antigen nucleotide sequence SEQ ID NO:74.
WO200055351-A1.
                                                                                                                                                       D AAC98064 standard; cDNA; 1186 BP.

DE Human colon cancer antigen nucleotide sequence SEQ ID NO:74

PN WO20005531-A1.

PD 21-SEP-2000.

PA (HUMA)- | HUMAN GENOME SCI INC.
Percent Similarity: 29.39* Mismatches: 115

Query March: 15.03* Indels: 42

RESULT 1330

ID AAH35018 standard; cDNA; 1186 BP.

DE Human colon cancer antigen encoding cDNA SEQ ID NO:2100.

PD 05-APR-2001.
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116
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Human polynucleotide SEQ ID NO 1325.
WO200190304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACN43511 standard; cDNA; 1234 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA39064 standard; cDNA; 1130 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ID AAA3064 standard; cDNA; 1130 B
DE Human secreted protein gene 13
PN W0200017222-A1.
PD 30-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.37%
Query March:
RESULT 1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID AAX56516 standard; DNA; 274 EDE Human 2861301 DNA fragment.
PN WO9914241-A2.
PD 25-WAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Query March: 1336
RESULT 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID ACN43511 standard; cDNA; 123
DE Human diagnostic and therape
PN WO200402377-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 43.94*
Best Local Similarity: 28.37*
Query Match: 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID ADF83096 standard; CDNA; 981
DE Human corticol thymocyte ree
PN WO2003100000-A2.
PD 04-DEC-2003.
PA (TULA-) TULARIK INC.
Percent Similarity: 28.81%
Best Local Similarity: 28.81%
Query Match: 14.83%
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29.39%
15.03%
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Human 2861301 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                   ID AAH35018 standard; of Human colon cancer by WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME Percent Similarity; gest Local Similarity;
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RESULT 1332
RESULT 1328
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RESULT 1331
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Anglogenesis differentially expressed gene GS-N52.
FR2836687-A1.
05-SEP-2003.
(GENE-) GENE SIGNAL.
(ALMA/) AL MAHMOOD S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP73100 standard; DNA; 8546 BP.
Angiogenesis inhibitor human DNA sequence, GS-N52.
FR2843753-A1.
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Mismatches:
    AAA39087 standard; cDNA; 1135 BP.
Human secreted protein gene 13 SEQ ID NO:46.
WO200017222-A1.
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Human NOV25b CG93858-02 DNA SEQ ID 85.
WO200281625-A2.
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RESULT 1342
ID AD008772 standard; cDNA; 15659 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADS09799 standard; DNA; 8546 BP.
Human therapeutic DNA - SEQ ID 36.
ADK60778 standard; DNA; 8546 BP.
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PN FR2836666-A1.

PD 05-SEP-2003.

PA (GENE-) GENE SIGNAL.

PA (ALMA/) AL MAHMOOD S.

Percent Similarity: 38-98*

"Acth: "Atch: 13.89$
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US2004018594-A1.
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Best Local Similarity: 29.24%
Query Match: 13.89%
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Local Similarity: 29.24%
Match: 13.89%
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Human thrombospondin protein, BTL.012, coding sequence WO200174852-A2
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DNA encoding novel human diagnostic protein #3924.
WO200175067-A2.
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WO2003102155-A2.
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Mismatches:
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RESULT 1347

ID ADL9396 standard; CDNA; 5877 BP.

DE Human G-coupled protein receptor-rele
PN US200406205-A1.

PA (LILL/) LI L.

PA (LILL/) LI L.

PA (GERL/) GERIACH V.

PA (MILL/) MILLER C.

PA (MILL/) SPYTEK R.A.

PA (SPYT/) SPYTEK R.A.

PA (SERH/) SERHUSEN B.D.

PA (SERH/) SENHUSEN B.D.

PA (SHEN/) SHENOY G.

PA (SHEN/) SHENOY G.

PA (SHEN/) SHENOY G.

PA (SHEN/) SHENOY G.

PA (SASWA) CASWAN G.

PA (CASWA) CASWAN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACA10120 standard; cDNA; 15660 BP. Human NOVX polynucleotide #10. WO200290504-A2.
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ID ADH72105 standard; DNA; 15660 BP.
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RESULT 1346
ID AAI72024 standard; CDNA; 4073
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PD 11-OCT-2001.
PA (FARB) BAYER CORP.
Percent Similarity: 38 98*
Best Local Similarity: 29.24*
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LILL/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (SHEW/) SHEWOY S G.
PA (TAUP/) TAUPIER R J.
PA (VOSS/) VOSS E Z.
PA (VOSS/) VOSS E Z.
PA (COSS/) VOSS E Z.
PA (CONSS/) VOSS E Z.
PA (CONS
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PA (CURA-) CURAGEN CORP.

38.98*

Percent Similarity: 38.98*

Best Local Similarity: 29.24*
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PA (HYSE-) HYSEQ INC.

Percent Similarity:

Best Local Similarity:
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Human gene of the invention NOV43d SEQ ID NO:1003.
WO2003102155-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADK60455 standard; DNA; 18207 BP.
Angiogenesis differentially expressed gene GS-N29.
FR2836687-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANK60756 standard; DNA; 18207 BP.
Angiogenesis differentially expressed gene GS-N29.
FR2836686-Al.
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Human NOV25c CG56914-03 DNA SEQ ID 87.
WO200281625-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABQ86156 standard; DNA; 16908 BP.
NOvel human gene. SEQ ID 27.
W0200250105-Al.
27-UUN-2002.
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PA (SMIK ) SMITHKLINE BEECHAM PLC.
PA (GLAX ) GLAXO GROUP LTD.
Percent Similarity: 38.98%
Best Local Similarity: 29.24%
Ouery Match: 13.83%
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PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMAL) AL MAHMOOD S.
Percent Similarity: 38.98*
Best Local Similarity: 29.24*
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PD 17-OCT-2002.
PO CURA) CURAGEN CORP.
Percent Similarity: 38.98%
Best Local Similarity: 29.24%
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pd 11-0cc2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.98%
Best Local Similarity: 29.24%
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13.83%
VOSS E Z.
VERNET C A.
MACDOUGALL J R.
                                                                                                      PATTURAJAN M.
BURGESS C E.
SHIMKETS R A.
TAUPLER R J.
                                                      ANDERSON D W.
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(GENE-) GENE SIGNAL.
(ALMA/) AL MAHMOOD S.
                                                                  ZHONG M.
MEZES P S.
FURTAK K.
                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                         MAZUR A.
                                                                                                                                  (MALY/)
(SHIM/)
(TAUP/)
(EDIN/)
                             (MACD/)
(RAST/)
(ANDE/)
(ZHON/)
                                                                                                         (PATT/)
(BURG/)
                                                                                (MEZE/
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PA (ROSE-) PA (NECA-) Percent Simil	Dest Docat of Query Match: RESULT 1362 ID ADR66513 DE Human pr		PA (HERM/) PA (PILA/) Percent Simil Best Local Si	Ž B		PA (HEKM/) PA (PILA/) Percent Simil Best Local Si Query Match:	150-21 1D ABT31932 DE Human br PN W0200300	it de	ID ABV76135 ID ABV76135 DE Coxsacki PN WO200287	it st	RESULT 1366  ID ADN95227  DE Human BE PN WO20309  PD 02-OCT-2	at G	Query Match: RESULT 1367 ID ABL88211 DE Human PR	rce st sry	1D ABL9570C DE Human ar PN WO20020B PD 31-JAN-2
23 81 63	. 62	23 81 63		41 124 42	à	41 124 42		47 114 49	(HCAR) CDNA.	42 109 49		47 114 49	ing cDNA.	47 114 49	
Conservative: Mismatches: Indels:	seguence, GS-N2	Conservative: Mismatches: Indels:	BP. CDNA SEQ ID NO 72.	Conservative: Mismatches: Indels:	in SEQ ID NO 72	Conservative: Mismatches: Indels:	) 11.	Conservative: Mismatches: Indels:	H BP. and Ad5 receptor (F	Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:	cor (CAR) encoding	# GES MBH. Conservative: Mismatches: Indels:	. 298 .
38.98% 29.24% 13.83%	DNA; 18207 BP. itor human DNA	38.98% 29.24% 13.83%		ME SCI INC. 40.93% 26.33% 13.60%	cDNA; 1853 BP. Ig a novel protein	ME SCI INC. 40.93% 26.33% 13.60%	DNA; 1536 BP. 1-01 DNA SEQ II	)RP. 42.40% 25.80% 13.44%	cDNA; 2354 BP	ORK STATE. 42.12% 26.74% 13.44%	CDNA; 2434 BP	UNIV TECHNOLOGY CORP. Larity: 42.40% Emilarity: 25.80%	cDNA; 2434 BP. lenovirus receptor	NOVARTIS AG. NOVARTIS-ERFINDUNGEN VERW GES MBH Larity: 42.40% Conserva imilarity: 25.80% Mismatch 13.44% Indels:	DNA; 2434 BP. mosis marker #598
Percent Similarity: Best Local Similarity: Query Match:	resold 1207 BP.  ID ADP73078 standard; DNA; 18207 BP.  DE Angiogenesis inhibitor human DNA sequence, PN FR2843753-A1.  PD 27-FBE-2004.  PA (GENE/) GENE S.	rcel at l	RESULT 1355  ID AAGSBASG standard; cDNA; 1853 DE Human immunoglobulin encoding PN W0200155315-A2.	PD 02-AUG-2001. PA (HUMA-) HUMAN GENOME SCI Percent Similarity: 40.939 Best Local Similarity: 26.333 Query Match: 13.60	Ę	PD 24-APR-2003. PD (HUMA-) HUMAN GENOME SCI INC Percent Similarity: 40.93% Best Local Similarity: 26.33% Query Match:	ESSUL 1236 BP.  ID ARX5626 standard; DNA; 1536 BP.  DE Human NOV4a CG59871-01 DNA SEQ ID 11  PN W0200201625-A2.  DN 17-077-2002	2 7 7 7 7	ABSOLI 1330 ID AAV50429 standard; cDNA; 2354 BP DE Human coxsackievirus and Ad2 and PN WO9833819-Al.	rce st	RESULT 1359  ID AAC85813 standard; DE Human CAR CDNA. PN US6245966-B1. PD 12-JUN-2001.	(UYTE-) cent Simil st Local Si	KESULT 1360 ID ABL60622 standard; CDNA; 24 DE Human coxsackie-adenovirus PN W0200229072-A2.	(NOVS) (NOVS) (CONT Similar Local Signy Match:	DE ADR24737 standard; DNA; DE Breast cancer prognosis PN W02004065545-A2. PD 05-AUG-2004.

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reast cancer / ovarian cancer related coding sequence #39.00012-A2.
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Human angiogenesis related cDNA PRO5723 SEQ ID NO: 279.
WC200208284 A2.
31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47
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BEC/LEC-related gene sequence SeqID149.
080640-Al.
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PRO5723 cDNA sequence SEQ ID NO:279.
00690-A2.
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sievirus receptor nucleic acid.
-) ROSETTA INPHARMATICS LLC.
-) NETHERLANDS CANCER INST.
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Novel human secreted and transmembrane protein PRO5723 cDNA.
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Human PR05723 nucleotide sequence SEQ ID NO:504
WO20007454-Al.
07-DEC-2000.
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ID ABK33643 standard; CDNA; 3060 BP.
DE CDNA encoding human PRO protein, Seq ID No 215.
PN W0200208288-A2.
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Human DNA82361 cDNA encoding PRO5723.
US2002192752-Al.
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AAD02924 standard; cDNA; 3060 BP.
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ID AAC91489 standard; cDNA; 3060 BP.
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WO200116319-A2.
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PA (GETH ) GENENTECH INC.
Percent Similarity: 42.4
Best Local Similarity: 25.8
                                                                                                          GERRITSEN M E.
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GURNEY A L.
HILLAN K J.
MARSTERS S A.
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(GETH ) GENENTECH INC.
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STEPHAN J F.
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Percent Similarity: 4
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WO200073452-A2.
                                                          FERRARA N.
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(WILL/) WILLIAMS P
(WOOD/) WOOD W I.
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ACA68604 standard; cDNA; 3060 BP.
Novel human secreted and transmembrane protein PRO5723 cDNA.
US2003088063-A1.
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US2003022187-A1.
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Novel human secreted and transmembrane protein PRO5723 cDNA.
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Novel human secreted and transmembrane protein PRO5723 CDNA.
US2002177148-A1.
28-NOV-2002.
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Novel human secreted or transmembrane protein PRO3301 DNA.
US2003027985-A1.
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Human sectreted/transmembrane protein cDNA, #177.
US200214961-A1.
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ABX80973 standard; cDNA; 3060 BP.
Human secreted/transmembrane protein cDNA, #177.
US2003027162-A1.
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CDNA encoding human PRO5723 polypeptide.
22002125576-Al.
12-SEP-2002.
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ABX17256 standard;
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RESULT 1381
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DE Human cDNA encoding secreted/transmembrane protein PRO5723.  PN US2003059832-A1.  PD 27-MAR-2003.  Percent Similarity: 42.40% Conservative: 47  Best Local Similarity: 25.80% Mismatches: 114  Query Match: 13.44% Indels: 49  RESULT 1393  ID ADAS 38945 standard; cDNA, 3060 BP.  DR Himan CDNA encoding secreted/transmembrane protein PRO5723.	US2003059780-A1. 27-WAR-2003. 27-WAR-2003. 27-WAR-2003. 27-WAR-2003. 27-WAR-2003. 28-WAR-2003. 25-80% Mismatches: 11 25-80% Mismatches: 13 25-80% Mismatch	PD 05-2023027988-A1. PD 06-EEB-2003 PA (GETH.) GENENTECH INC. Percent Similarity: 42.40\$ Conservative: 47 Best Local Similarity: 25.80\$ Mismatches: 114 Query Match: 13.44\$ Indels: 49 RESULT 1395 ID ADA93066 standard; CDNA; 3060 BP. DE Human cDNA encoding secreted/transmembrane protein PRO5723.	at ce	06-MAR-2003. (GETH ) GENENTECH INC. crent Similarity: 42.40% Mismatche st Local Similarity: 25.80% Mismatche sry March: 13.44% Indels: MATH 1397 ACH65628 standard; CDNA; 3060 BP.	DE Human CDNA encoding secreted/transmembrane protein FROS/23.  PN US2003044806-A1.  PD 06-MAR-2003.  Percent Similarity: 42.40\$ Conservative: 47  Best Local Similarity: 25.80\$ Mismatches: 114  Query Match: 13.44\$ Indels: 49  RESULT 1398  ID ADA22627 standard; cDNA; 3060 BP.  DE Human cDNA encoding secreted/transmembrane polypeptide PRO572	gir tr	erce SUI SUI Sury
Conservative: 47 Mismatches: 114 Indels: 49 p.	Conservative: 47 Mismatches: 114 Indels: 49 P.	Conservative: 47 Mismatches: 114 Indels: 49	Conservative: 47 Mismatches: 114 Indels: 49 2.	Conservative: 47 Mismatches: 114 Indels: 49 Ansmembrane polypeptide PRO5723.	Conservative: 47 Mismatches: 114 Indels: 49 p. ansmembrane protein, PRO5723.	Conservative: 47 Mismatches: 114 Indels: 49 2.	Conservative: 47 Mismatches: 114 Indels: 49 p. ansmembrane protein PRO5723. Conservative: 47 Mismatches: 114 Indels: 49
PA (GETH ) GENENTECH INC.  Percent Similarity: 42.40% Conservatives to cal Similarity: 25.80% Mismatches Query March: 13.44% Indels: RESULT 1384 Indels: DD ACA88560 standard; cDNA; 3060 BP.  DE Human secreted and transmembrane polypeptide PD US2002197615-A1.	PA (GETH) GENENTECH INC.  Percent Similarity: 42.40% Conse.  Best Local Similarity: 25.80% Misma Query Match: 13.44% Indell  RESULT 1385  DE CDNA encoding human PRO5723 polypeptide PN 022003017981-A1.	PD 23-JAN-2703, PD 23-JAN-2703, PB 22-CAN-2703, Beet Local Similarity: 25.80% Query Match: REGULT 1386 ID ABT44333 standard; CDNA; 3060 BP DE Human PRO5723 CDNA. PN US2003050448-A1. PD J3-MAR-27003. PA (GRTH ) GENEWTECH INC	ccent Simil st Local Si st Local Si sty Match: SULT 1387 ADA38015 Human CD US200300	rce st sury Sur	PN USZU03054044-A1. PD 20-MAR-2003. Percent Similarity: 42.40% Conserva: Best Local Similarity: 25.80% Mismatch Query Match: 13.44% Indels: RESULT 1389 ID ADA10488 standard; cDNA; 3060 BP. DE Human cDNA encoding secreted/transmembrane DN USZ003059831-A1.	in i	st sur

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INC.  42.40% Mismatches: 13.44% Indels: cDNA; 3060 BP. cd and transmembrane protein PR 25.80% Mismatches: 13.44% Indels: cDNA; 3060 BP. cd and transmembrane protein PR 25.80% Mismatches: 13.44% Conservative: 25.80% Mismatches: 13.44% Conservative: 25.80% Mismatches: 13.44% Conservative: 25.80% Mismatches: 13.44% Conservative: 25.80% Mismatches: 13.44% Indels: cDNA; 3060 BP. ccide #141. Conservative: 25.80% Mismatches: 13.44% Conservative: 25.80% Mismatches: 13.44% Mismatches: 13.44% Conservative: 25.80% Mismatches: 13.44% Mismatches: 13.44% Conservative: 25.80% Mismatches: 13.44% Indels: cDNA; 3060 BP. ccide #141. Conservative: 25.80% Mismatches: 11NC. 42.40% Mismatches: 13.44% Indels: 11NC. 25.80% Mismatches: 13.44% Indels: 13.44% Indels: 13.44% Indels:	47 114 49	n PRO5723.	47 114 49	47 114 49		47 114 49	47 114 49		47 114 49	47 114 49	47 114 49
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#33951 standard; cDNA; 3060 BP.
el human secreted and transmembrane protein PRO5723 cDNA.
a03069397-Al.
APR-2003.
TH ) GENENTECH INC.
Similarity: 42.40$ Conservative: 47
Almilarity: 25.80$ Mismatches: 114
tch: Indels: 49
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el human secreted and transmembrane protein PRO5723 cDNA.
003092887-Al.
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an cDNA encoding secreted/transmembrane protein PRO5723.
003049681-A1.
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Laman PRO polynucleotide #141.

22003045463-Al.

5-MAR-2003.

5-MAR-2003.

5-MILIARITY: 42.40% M

Agtch: 13.44% I
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an PRO polynucleotide #141.
003027754-A1.
FEB-2003.
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an PRO polynucleotide #141.
003064375-Al.
APR-2003.
                                                                                       87254 standard; cDNA; 3060 BP.
an PRO polynucleotide #108.
003088067-A1.
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an PRO polynucleotide #108.
003092890-A1.
,-MAY-2003.

SETH ) GENENTECH INC.

t Similarity: 42.40%

coal Similarity: 25.80%
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Best Local Similarity:
Query Match:
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05288-A1.

PN US200310 PD 05-JUN-2 PA (GETH) O	ery Match SULT 142 ADD08:	DE NOVEL DU PN US200306 PD 10-APR-2 Percent Simil	Query Match: RESULT 1428 ID ADC82161 DE Human PR	PN 05200308 PD 01-MAY-2 Percent Simil Best Local Si	Query Match: RESULT 1429 ID ADD07803 DE Novel hu PN US200219	PA (GETH) Percent Simil Best Local Si	ŽĮ.	PD 22-MAY-2 PA (GETH) Percent Simil Best Local Si	Ç Ç	PD 27-MAR-2 Percent Simil. Best Local Sil Query Match:	ID ADD06397 ID ADD06397 DE NOVEl hu PN US200307 PD 17-APR-2 DA (GT-APR)	st ery	ID ADD10568  DE Human see PN US200310 PD 05-JUN-2 PA (GETH )	rce st ] ery	RESULT 1434  ID ADD08674  DE NOVEL hu PN US200307  PD 17-APR-2	rce st
in PRO5723.	47 114 49		47 114 49		47 114 49	PRO5723 cDNA.	47 114 49	RO5723 cDNA.	47 114 49	PRO5723 cDNA.	47 114 49	ROS723 cDNA.	47 114 49	PRO5723 cDNA.	47 114 49	RO5723 CDNA.
:DNA; 3060 BP. secreted/transmembrane protein PRO5723	Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:	3060 BP. transmembrane protein P	Conservative: Mismatches: Indels:	3060 BP. transmembrane protein PRO5723	Conservative: Mismatches: Indels:	3060 BP. transmembrane protein P	Conservative: Mismatches: Indels:	3060 BP. transmembrane protein PRO5723	Conservative: Mismatches: Indels:	3060 BP. transmembrane protein P	Conservative: Mismatches: Indels:	3060 BP. transmembrane protein PRO5723
CDNA; 3060 BP.	42.40% 25.80% 13.44%	; cDNA; 3060 BP. leotide #108.	INC. 42.40% 25.80% 13.44%	cDNA; 3060 BP.	INC. 42.40% 25.80% 13.44%		INC. 42.40% 25.80% 13.44%		INC. 42.40% 25.80% 13.44%	cDNA; ed and	INC. 42.40% 25.80% 13.44%		INC. 42.40% 25.80% 13.44%		42.40% 25.80% 13.44%	
RESULT 1418 ID ADC11682 standard; C DE Human CDNA encoding PN US2003069403-A1.	PD 10-APR-2003. Percent Similarity: Best Local Similarity: Ouery Match:	KESULT 1419 ID ADC36944 standard; DE Human PRO polynucl PN US2003088065-A1. PD 08-MAV-2003	PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	ADC21934 standard, Human PRO polynuc] US2003096969-A1.	PD 22-MAX-2003.  PD 62FT4) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	ADC49965 standard Novel human secre US2003088064-Al.	PD 08-MAY-2003. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	RESULT 1422 ID ADC49164 standard; CDNA; DE NOVEL human secreted and PN US2003088070-A1.	PD 08-MAY-2003. PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	1 standard; uman secret 88071-A1.	PA (GETH) GENERATECH Percent Similarity: Best Local Similarity: Ducry Match:	ID ADC47542 standard; cDNA; DE Novel human secreted and PN US2003088072-A1.	ary at	DE Novel human secreted and PN US2003082546-A1.	PD 01-MAY-2003. Percent Similarity: Best Local Similarity: Query Match: RESULT 1426	nbsour 1420 ID ADC47287 standard; cDNA; DE Novel human secreted and

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6 standard; cDNA; 3060 BP.
uman secreted and transmembrane protein PRO5723 cDNA.
68623-A1.
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Numan secreted and transmembrane protein PRO5723 cDNA.
073090-Al.
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1.arity: 42.40% Conservative: 47
Similarity: 25.80% Mismatches: 114
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uman secreted and transmembrane protein PRO5723 cDNA.
93299-A1.
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uman secreted and transmembrane protein PRO5723 cDNA.
96972-A1.
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uman secreted and transmembrane protein PRO5723 cDNA.
73816-A1.
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ecreted/transmembrane PRO polypeptide cDNA #140.
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o DNA.		CDNA.						cDNA.		cDNA.		cDNA.			
			47 114 49	CDNA #140.	47 114 49		47 114 49		47 114 49	PRO5723 c	47 114 49	PRO5723 c	47 114 49		47 114 49
brane orotein PRO5723		3060 BP. transmembrane protein PRO5723	Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:	3060 BP. transmembrane protein PRO5723	Conservative: Mismatches:. Indels:	3060 BP. transmembrane protein Pl	Conservative: Mismatches: Indels:	3060 BP. transmembrane protein Pl	Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:
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DNA;	1C. 12.40% 13.44%		INC. 42.40% 25.80% 13.44%	cDNA; insmembra	42.40% 25.80% 13.44%	cDNA;	42.40% 25.80% 13.44%		INC. 42.40% 25.80% 13.44%		INC. 42.40% 25.80% 13.44%		INC. 42.40% 25.80% 13.44%	cDNA;	42.40% 25.80% 13.44%
RESULT 1435 ID ADC77916 standard; cl DE Novel human secreted	PN US2003088066 A1. PD 08-MAY-2003. PA (GETH ) GENENTECH Similarity: Best Local Similarity: Query Match:	RESULT 1436 ID ADD07123 standard; cDNA; DE Novel human secreted and PN US2002193300-A1.	-2002. ) GENENTECH ilarity: Similarity:	ard; /tra 1. ECH	arity: milarity:	KESULI 1438 ID ADC83370 standard; CDNA; DE Human PRO polymucleotide PN US2003055783-A1.	PD 27-MAK-2003. Percent Similarity: Best Local Similarity: Query Match:	RESULT 1439 ID ADD50879 standard; CDNA; DE Novel human secreted and PN US2003105291-A1.	(GETH ) GENENTECH cent Similarity: st Local Similarity: sty Match:	ID ADD15379 standard, cDNA, DE Novel human secreted and PN US20030639437-A1.	(GETH ) GENENTECH COENT Similarity: bt Local Similarity: sty Match:	ID ADD51125 standard; cDNA; DB Novel human secreted and PN US2003105290-A1	-2003. ) GENENTECH ilarity: Similarity:	ADD55477 standard; Human PRO polynucl US2003077593-A1,	FD 44-AFK-2003. Percent Similarity: Best Local Similarity: Ohery Match.

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371 standard; cDNA; 3060 BP.
human secreted and transmembrane protein PRO5723 cDNA.
3105289-A1.
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human secreted and transmembrane protein PRO5723 CDNA.
3087305-A1.
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CDNA encoding secreted/transmembrane protein PRO5723.
3068647-Al.
R-2003.
secreted/transmembrane PRO polypeptide cDNA #140.
N-2003.
N-2003.
milarity: 42.40% Conservative: 47
milarity: 25.80% Mismatches: 114
similarity: 13.44% Indels: 49
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nn PRO polynucleotide #141.

002132253-A1.

ERP-2002.

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13.44%
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PRO polynucleotide #108.
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SIMILARILY: 42.404

Similarity: 25.804

al Similarity: 13.448
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FH ) GENENTECH INC.

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36635-A1.

	25.80% 13.44%	Mismatches: Indels:	114 49	PN US2003036 PD 20-FEB-20 PA (GETH ) C
Standard; 05723 nucle	cDNA, 3060 BP. eotide sequence	SEQ ID NO:504.		rcer st 1
ž ë	INC. 42.40% 25.80% 13.44%	Conservative: Mismatches: Indels:	47 1114 49	Tos
T 1453 ADE94084 standard; cDNA; Immune disease treatment, US2003082199-A1.	NA; 3060 BP. nent/diagnosis related	s related PRO57	PROS723 CDNA.	PA (GETH ) C Percent Simils Best Local Sin Query Match:
PA (GETH) GENENTECH INC Percent Similarity: 42 Best Local Similarity: 25 Query Match: 13 RESULT 1454 ID ADI35685 standard; CD	3060 BP.	Conservative: Mismatches: Indels:	47 114 49	KESULI 1462 ID ID CDNA encc PN US2002102 PD (GFH) ( PA (GFH) ( Percent Simile
U .		Conservative: Mismatches: Indels:	47 114 49	" <u>"</u> " "
andard; secrete 2-Al.	cDNA, 3060 BP. ed and transmemb	3060 BP. transmembrane protein PRO5723	RO5723 CDNA.	PD 15-MAY-20 PA (GETH ) G Percent Simila Best Local Sim
003. arity: milarity: standard; O polynucle	42.40% 25.80% 13.44% CDNA, 3060 BP.	Conservative: Mismatches: Indels:	47 114 49	Query Match: RESULT 120 DD ADE21089 DB NOVEL hum PN 29-MAY-20 PD 29-MAY-20 PD 40-MAY-1
	42.40% 25.80% 13.44%	Conservative: Mismatches: Indels:	47 114 49	# 4.5
		3060 BP. transmembrane protein PRO3301	03301 DNA.	DE Human PRC PN US2003100 PD 29-MAY-20 PA (GETH ) C Percent Simila
ETH ) GENENTECH INC Similarity: 42 cal Similarity: 25 atch: 13	INC. 42.40% 25.80% 13.44%	Conservative: Mismatches: Indels:	47 114 49	Best Local Sin Query Match: RESULT 1466 ID ADD75162
JI 1438 ACA69375 standard; cDNA; 3060 BP. Human cDNA encoding secreted/transmembrane USZ003032023-A1.	NA; 3060 BP. secreted/trans	smembrane prote	protein PROS723.	DE HUMAIN PKC PN US2003100 PD 29-MAY-20 PA (GETH )
FD 13-FEB-2003.  Best Local Similarity: 42  Best Local Similarity: 25  Query Match: 13	42.40% 25.80% 13.44%	Conservative: Mismatches: Indels:	47 114 49	Percent Simila Best Local Sin Query Match: RESULT 1467
<pre>5 standard; ecreted/trar 50384-Al.</pre>	CDNA; 3060 BP. 18membrane prote	ein cDNA, #177.		ID ADD75908 DE Novel hum PN US2003100 PD 29-MAY-20
PA (GETH) GENENTECH INC. Percent Similarity: 42. Best Local Similarity: 25. Query Match: 13.	INC. 42.40% 25.80% 13.44%	Conservative: Mismatches: Indels:	47 114 49	gr, r.ce
RESULT 1460 ID ACA66948 standard; cDNA; 3060 BP. DE cDNA encoding human PRO polypeptide #108	NA, 3060 BP. PRO polypeptic	le #108.		ID ADD85140 DE Novel hum PN US2003100

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O standard; cDNA; 3060 BP.
uman secreted and transmembrane protein PRO5723 cDNA.
45687-A1.
2003.
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uman secreted and transmembrane protein PRO5723 cDNA.
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uman secreted and transmembrane protein PRO5723 cDNA.
00717-A1.
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SETH ) GENENTECH INC.

5. Similarity: 42.40% Mismatches: 114

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CD683717 EST237 hu
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BF916759 ILI3-UTF011
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Genoscope.

Direct Submission

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 1919 19106 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
         21-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGlyGlyAsnSerTyrGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaSerTyrGluAspArgValThrPheLeuProThrGlyIleThrPheLysSerValThr 100
                                                           HTC; CNSLT_cDNA.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1594)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
         CR617107 1594 bp mRNA linear HTC 21-JUL-200
full-length cDNA clone CS0D1075YL24 of Placenta Cot 25-normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                  25-normalized"
                                                                                                                                                                                                                                                                                                                                                                                                                  1594
294
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                   CR617107.1 GI:50497914
                               of Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                       GCTTCCTATGAGGACCGGGGGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGGGACA
                                                                                                                                                                                                                                                                                                                                   ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGlyGlyAsnSerTyrGly
                                                                                                                                                                                                                                                                                                                                                 CGGGAAGACACTGGGACATACACTTGTATGGTCTCTGTGAGGAAGGCGGCAACAGCTATGGG
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                                                                                                                                                                                                                                                    GluTrpLysPheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnLysIleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArgalaPheSerAsnSerSerTyrValLeuAsnProThrThrGlyGluLeuValPheAsp
                               1514
294
0
2
3
                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                  Gaps:
                                                                                                       (1-1514)
                                                                                                       US-10-785-220B-1 (1-299) x CR617300
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1504.50
98.33%
98.33%
97.44%
                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                     Alignment Scores:
Pred. No.:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; F 1 (bases 1 to 1020)

B 1 (bases 1 to 1020)

NIH-MGG http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Ontact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:

http://image.llhl.gov

Plate: LiAM12756 row: m column: 22

High quality sequence stop: 666.
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1020 bp mRNA linear EST 20-FEB-2002
AGENCOURT 6543385 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5740989
5/, mRNA Fequence.
BM548873
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                   320 CGGGAAGACACTGGGACATACACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGG
                                                                                                                                                                       GluValLysValLysLeuIleValLeuValProProSerLysProThrValAsnIlePro
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                                                                                                                                                                                                                                                                                                                                                                                                                               CGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACAACAGGAGAGACTGGTCTTTGAT
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                                                                                               ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGlyGlyAsnSerTyrGly
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
End alls tstrand CDNA was primed with a Not1 coligo (dT) primer. Fr
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CSODL004CB02QP1&c=250.r.
                                                                                           ALS60725
ALS60725 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED Homo sapiens cDNA clone CSODL004YD03 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Bases 1 to 993)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization (Dnbblished (2001)
On Peb 15, 2001)
Con Peb 15, 2001
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/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
ATGGGGACAAAAGGCGCAAGTCGAGAAGAACTGTTGTTCATATTGGCGATCCTG
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODL004YD03"
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMYSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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AL553289 3 GI:45858058
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31275103.

Contact: Genoscope
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-Oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                 TyrSerArgGlyHisPheAspArgThrLysLysGlyThrSerSerLysLysVallleTyr
                                                                                                                                  198 TATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGACTTCGNAGTAGAAGGTGATTTAC
                              GCAGCCGTCCTTGTAACCCTGATTCTCCTGNGAAATCTGGTTTTTGGCATCTGGTTTGCC
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AlaAlaValLeuValThrLeuIleLeuLeuGlyIleLeuValPheGlyIleTrpPheAla
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODIO?5DF12QP1&c=250.r.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI075YL24"
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/organism="Homo sapiens"

/mol_type="mRNA"

/db xref="texon:9606"

/clone="IMAGE:6481188"

/tismue_type="carcinoma, cell line"

/tab host="DH10B (phage-resistant)"

/clone lib="NIH MGC_40"

/clone lib="NIH MGC_40"

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Note: this is a NIH_MGC Library."
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                  can
DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LiML at: http://image.llnl.gov column: 13 Plate: LLCM2662 row: c column: 13 High quality sequence stop: 685. Location/Qualifiers
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BQ928243 GI:22343274
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National Libritutes of Health, Mammalian Gene Collection (MGC) (Mnpublished (1999))

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/TTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                 GluTrpLysPheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnLysIleThr
                                                                                              GAGTGGAAGTTTGACCAAGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACA
                                                                                                                                AlaSerTyrGluAspArgValThrPheLeuProThrGlyIleThrPheLysSerValThr
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                                                                                                                                                                                                                                                                           HTC 21-JUL-2004
25-normalized
                                                                                                                                                        AlaAlaValLeuValThrLeuIleLeuLeuGlyIleLeuValPheGlyIleTrpPheAla 260
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1 (bases 1 to 1488)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
                     598 CGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACAACAGGAGAGCTGGTCTTTGAT
                                                                                                                           GCAGCCGTCCTTGTAACCCCTGNNATCTCTGNGAATCTTGGTTTTTGGCATCTGGTTTTGCC
                                                                 ProMetThrSerAsnAlaValArgMetGluAlaValGluArgAsnValGlyValIleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                1488 bp mRNA linear full-length cDNA clone CSODI032YK05 of Placenta Cot Of Howo sapiens (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/mol_txpe="mRNA"
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/clone="GSOD1012xK05"
/tissue type="Placenta Cot 25-normalized"
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CR608619.1 GI:S0489426
HTC; CNSLT_CDNA.
HOMO BADIENS (human)
HOMO BADIENS
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Query Match:
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MetGlyThrLysAlaGlnValGluArgLysLeuLeuCysLeuPheIleLeuAlaIleLeu 20

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mRNA linear EST 21-AUG-2002 sapiens cDNA clone IMAGE:6480623
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 886)
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                                                                                                  157 TTGTGCTCCCTGGCATTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATT
                                                                                                                                                                                                     CCTGAGAATAATCCTGTGAGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTG
                                                                                                                                                                                                                                                                      GluTrpLysPheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnLysIleThr
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                                                                           LeuCysSerLeuAlaLeuGlySerValThrValHisSerSerGluProGluValArgIle
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AUTHORS
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657 220 717 240

597

777

837

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Genoscope - Centrer National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequeréfégenoscope.cns.fr, Web : www.genoscope.cns.fr,
End characteréfégenoscope.cns.fr, Web : www.genoscope.cns.fr
End cDNA was primed with a Not1--oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B96 bp mRNA linear EST 27-APR-2004 BX379273 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA CLONE CSODI032YK05 5-PRIME, mRNA sequence.
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primer. Five prime end enriched, double-strand cDNA was
digested with NotI and cloned into the NotI and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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1 (bases 1 to 80 pt.

11, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization (Dnpublished (2001)

On May 8, 2003 this sequence version replaced gi:30456760.

Contact: Genoscope
                               ProLeuSerAlaSerAspThrGlyGluTyrSerCysGluAlaArgAsnGlyTyrGlyThr
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/mol_type="mRNA"
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/db_txef="txxxon:9606"
/clone="tMAGE:64806023"
/tissue_type="carcinoma, cell line"
/tasue_type="carcinoma, cell line"
/clone lib="NHH MGC 40"
/clone lib="NHH MGC Calcoma, pyriming, cell forlioma, cell cell forlioma, cel
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                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabe-ramail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://amage.llnl.gov
Plate: LLCM2660 row: k column: 24
High quality sequence stop: 698.
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   Vational Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clome_lib="NIH_MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
/note: constructed by ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis Kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I:M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2660 row: c column: 15

High quality sequence stop: 692.
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     1 (bases 1 to 907)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
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                                                                                      MetGlyThrLysAlaGlnValGluArgLysLeuLeuCysLeuPheIleLeuAlaIleLeu
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5, mRNA fequence.
BQ928239
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Length:
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Conservative:
Mismatches:
Indels:
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     6.27e-133
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96.06%
95.70%
85.10%
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Query Match:
DB:
                   Percent Similarity:
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BU542115 GI:22852598
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                                                                                                  AlaalaValLeuValThrLeuIleLeuLeuGlyIle-LeuValPheGlyIleTrpPheAl 260
                                                                                                                                          781 GCAGCCGTCCCTGTAACCCTGATTCTCCTGGAATCTTTGGTTTTTTGGCATCTGGTTTTG 840
                                                                                                                                                       260 a---TyrSerArgGlyHis-PheAspArgThrLys---LysGlyThrSerSerLysLys 277
                                                                                                                                                               ProSerGluTyrThrTrpPheLysAspGlyIleValMetProThrAsnProLysSerThr
                            CCTTCTGAATACACCTGGTTCAAAGATGGGATAGTGATGCCTACGAATCCCCAAAAGCACC
                                                                        ProLeuSerAlaSerAspThrGlyGluTyrSerCysGluAlaArgAsnGlyTyrGlyThr
                                                                                      CCCCTGTCAGCCTCTGATACTGGAGAATACAGCTGTGAGGCACGGAATGGGTATGGGACA
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       481
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AGENCOURT 6924454 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5813758 5', mRNA sequence.
BQ057979 GI:19817319
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                                                                                                                                                                                                                                                                                                                                                             TCCTCTGCCACCATTGGGAACCGGGCAGTGCTGACATGCTCAGAACAAGATGGTTCCCCA
                                                                                                                                                                                                                                                                                                                                                                                     ProSerGluTyrThrTrpPheLysAspGlyIleValMetProThrAsnBroLysSerThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetGlyThrLysAlaGlnValGluArgLysLeuLeuCysLeuPhelleLeuAlaIleLeu
                                                                                                                                                                                                                                                                        101 ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGlyGlyAsnSerTyrGly
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CD384890 891 bp mRNA linear EST 30-MAY-2003
AGENCOURT 14286171 NIH_MGC_173 Homo sapiens CDNA 5', mRNA sequence.
CD384890
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                                                                                                                                                                                                                                                                                                                                                                                           ProMetThrSerAsnAlaValArgMetGluAlaValGluArgAsnVal-GlyValIleVa 240
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmlDA07 Bethesda, WD 20892
Email: cgapbs-remail.nih.gov.
Tissue Procurement: Dr. Jamie Thompson, University of WI
CDNA Library Preparation: Gina Zastrow-Hayes
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
                                                                                                                                                                                                                                                                                                                                       ProSerGluTyrThrTrpPheLysAspGlyIleValMetProThrAsnProLysSerThr
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                     GluValLysValLysLeuIleValLeuValProProSerLysProThrValAsnIlePro
                                                                                                                                  TCCTCTGCCACCATTGGGAACCGGGCAGTGCTGACATGCTCAGAACAAGATGGTTCCCCA
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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High quality sequence stop: 703.
Location/qualifiers
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CD384890
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                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1039)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                Email: cgapBe-remail.nih.gov
Tissue Procurement: Low Standt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Flate: LLCM2066 row: e column: 23
High quality sequence stop: 716.
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90.94%
89.32%
84.81%
                                          Homo sapiens
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/Listue_type=carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                BQ887533 878 bp mRNA linear EST 16-AUG-2002
AGENCOURT 8675238 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6380256
5, mRNA Sequence.
BQ887533
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                                                                                                                                                                                                                                                                                                                                                                              Introducts Robert Strausberg, Ph.D.

Email: capaba-ramail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: WGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov
Plate: LLCM268 row: j column: 01

High quality sequence stop: 614.
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                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 878)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Matches:
Conservative:
Mismatches:
Indels:
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                   266
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                 259 -PheAlaTyrSerArgGlyHisPhe
                                                     854 TTGGCCTATAGGCCGAGGCCACTTT
                                                                                                                                                                                                            BQ887533.1 GI:22279547
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1281.00
95.60%
94.87%
82.97%
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Best Local Similarity:
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DB:
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KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 GAGTGGAAGTTGACCAAGAGAGACACCACAGACTCGTTTGCTATAATAACAAGATCACA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 AlaSerTyrGluAspArgValThrPheLeuProThrGlyIleThrPheLysSerValThr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTTCCTATGAGGACCGGGTGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGlyGlyAsnSerTyrGly 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCCTGTCAGCCTCTGATACTGGAGAATACAGCTGTGAGGCACGGAATGGGTATGGGACA 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProMetThrSerAsnAlaValArgMetGluAlaValGluArg-AsnValGlyValIleVa 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProGluAsnAsnProValLysLeuSerCysAlaTyrSerGlyPheSerSerProArgVal 60
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LIBR_PROVIDER - Bradfield"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     494 TCCTCTGCCACCATTGGGAACCGGGCAGTGCTGACATGCTCAGAACAAGATGGTTCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCATGACTTCAAATGCCGTGCGCATGGAAGCTGTGGGGGAAATGTGGGGTCATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 794 GGCAGCCCGTCCTTGTAACCCTGATTCTCCTGGGAATCTTGGGCTTTTTGGGCATCTTGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434 GAGGTCAAGGTCAAGCTCATCGTGCTTGTGCTCCATCCAAGCCTACAGTTAACATCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                554 CCTTCTGAATACACCTGGTTCAAAGATGGGATAGTGATGCCTACGAAATCCCAAAAGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgAlaPheSerAsnSerSerTyrValLeuAsnProThrThrGlyGluLeuValPheAsp
                                                         WA01
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                                                                                                                                                                                                                                                 891
262
1
3
3
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Conservative:
Mismatches:
Indels:
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	GGTTTGCCTATAGCCGAGGGCCACTTGAACAG 873	841	q
	p-PheAlaTyrSerArg-GlyHisPheAspArg 268	258	ò
  GGGCATCTG 840	. TGGGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGGAAATCTTGGGTTTTTGGGCATCTG	781	QQ
e-GlylleTr 258	ValAlaAlaValLeuValThrLeuIleLeuLeuGlyIleLeuValPhe-GlyIl	240	ò
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ValGlyValile 239	ProMetThrSerAsnAlaValArgMetGluAlaValGluArgAsn-	221	δ
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uValPheAsp 200	ArgAlaPheSerAsnSerTerTyrValLeuAsnProThrThrGlyGluLeuValPheAsp	181	ò
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OLYSSerThr 180	ProSerGluTyrThrTrpPheLysAspGly11eValMetProThrAsnProLysSerThr	161	ò
	. TCCTCTGCCACCATTGGGAACCGGGCAGTGCTGACATGCTCAGAACAAGATGGTTCCCCCA	481	qq
pGlySerPro 160	SerSerAlaThrIleGlyAsnArgAlaValLeuThrCysSerGluGlnAspGlySerPro	141	ò
TAACATCCCC 480	. GAGGTCAAGGTCAAGCTCATCGTGCTTGTGCTCCCATCCAAGCCTACAGTTAACATCCCC	421	g
Asn1 ePro 140	GluValLysValLysLeuIleValLeuValProProSerLysProThrValAsnIlePro	121	ò
CAGCTATGGG 420	. CGGGAAGACACTGGGACATACACTTGTATGTCTCTGAGGAAGGGGGCAACAGCTATGGG	361	qq
nSerTyrGly 120	. ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGluGlyGlyAsnSerT	101	ò
GICCGIGACA 360	. GCTTCCTATGAGGACCGGGTGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACA	301	q C
sSerValThr 100	AlaserTyrGluAspArgValThrPheLeuProThrGlylleThrPheLy	81	ò
CAAGATCACA 300	GAGIGGAAGTITGACCAAGGAGACACCACCAGACTCGTITGCTATAATAACAAGATCACA	241	q
nLysileThr 80	GluTrpLysPheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnLysIl	61	ò

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